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146933

From: Hamud, Fozia
Sent: Thursday, March 03, 2005 3:29 PM
To: STIC-Biotech/ChemLib
Subject: sequence search for 09/617,720

Please search SEQ ID NOs: 1, 2, 3 of 09/617,720 against commercial and interference data bases. thanks.

Fozia Hamud
Patent Examiner
Remsen 4D64
Mail Box: Remsen 4C70
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Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: 3/14 _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:56:15 ; Search time 137.39 Seconds

(without alignments)
11636.250 Million cell updates/sec

Title: US-09-617-720A-3

Perfect score: 42

Sequence: 1 aggaaggaggagaagga.....gagtgaaggaggagtga 42

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	858	BI090567	BI090567 602855674
2	42	100.0	985	AL545100	AL545100 AL545100
3	42	100.0	2605	CR613851	CR613851 full-length
4	34.6	82.4	818	BG787987	BG787987 SEAUWC007
C 5	33	78.6	643	AZ649302	AZ649302 IM0518F16
C 6	31.4	74.8	103	AI252833	AI252833 qv49f02.x
C 7	31.4	74.8	154	AZ022385	AZ022385 RPCI-23-3
C 8	31.4	74.8	156	CE100567	CE100567 tigr-gss-
C 9	31.4	74.8	161	AZ714952	AZ714952 RPCI-24-1
C 10	31.4	74.8	170	AQ980187	AQ980187 RPCI-23-3
C 11	31.4	74.8	346	AZ686613	AZ686613 2M0180H20
C 12	31.4	74.8	408	AQ628256	AQ628256 CITBI-EI-
C 13	31.4	74.8	424	AA794173	AA794173 vm67b07.r
C 14	31.4	74.8	514	AA684355	AA684355 vm69d08.r
C 15	31.4	74.8	524	CF998116	CF998116 A0234D08-
C 16	31.4	74.8	554	AZ296671	AZ296671 RPCI-23-1
C 17	31.4	74.8	560	AZ632723	AZ632723 IM0487G01
C 18	31.4	74.8	581	CF897840	CF897840 A0230F01-
C 19	31.4	74.8	585	BG802700	BG802700 0184-18 M
C 20	31.4	74.8	586	AZ709886	AZ709886 RPCI-24-6
C 21	31.4	74.8	609	B0749184	B0749184 UI-M-FD0-
C 22	31.4	74.8	629	CE381159	CE381159 tigr-gss-
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24	31.4	74.8	655	CE829872	CE829872 tigr-gss-

25	31.4	74.8	696	8	AZ319198
26	31.4	74.8	733	8	AZ748464
C 27	31.4	74.8	795	4	BI251681
C 28	31.4	74.8	1163	4	BI664455
C 29	31	73.8	854	8	AQ745575
C 30	30.8	73.3	183	6	CB606703
C 31	30.8	73.3	303	7	H32873
C 32	30.8	73.3	330	1	AA736512
C 33	30.8	73.3	346	6	C06764
C 34	30.8	73.3	424	8	BZ263903
C 35	30.8	73.3	435	4	BG667137
C 36	30.8	73.3	457	6	CB740130
C 37	30.8	73.3	471	2	BF522708
C 38	30.8	73.3	494	1	AI575683
C 39	30.8	73.3	562	8	AZ712287
C 40	30.8	73.3	586	8	BH256925
C 41	30.8	73.3	748	8	BZ771226
C 42	30.8	73.3	750	9	AG281713
C 43	30.8	73.3	825	8	BZ184962
C 44	30.8	73.3	967	8	CC247236
C 45	30.8	73.3	1229	9	CL079684

ALIGNMENTS

RESULT 1
BI090567
LOCUS 602855674F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996939 5',
DEFINITION mRNA sequence.
ACCESSION BI090567
VERSION BI090567.1 GI:14508897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 858)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11023 row: c column: 20
High quality sequence stop: 670.
Location/Qualifiers
source
1. .858
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4996939"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."

Query Match 100.0%; Score 42; DB 4; Length 859;

Best Local Similarity 100.0%; Pred. No. 0.046;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGA 42

```

|||||
63 AAGGAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAG 104

RESULT 2
AL545100 985 bp mRNA linear EST 25-MAR-2004
LOCUS AL545100 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI013YA07 5-PRIME, mRNA sequence.
ACCESSION AL545100
VERSION AL545100.3 GI:45745585
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 985)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31266936.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1383.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI013AA04QP1&c=1383.f.
FEATURES
source
1. 985
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI013YA07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 100.0%; Score 42; DB 1; Length 985;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAG 42
DB 31 AAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAG 72

RESULT 3
CR613851 2605 bp mRNA linear HTC 21-JUL-2004
LOCUS CR613851 full-length cDNA clone CSODI013YA07 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR613851
VERSION CR613851.1 GI:50494658
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2605)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2605)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 2605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI013YA07"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 100.0%; Score 42; DB 3; Length 2605;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAG 42
DB 31 AAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAG 72

RESULT 4
BG787987 818 bp mRNA linear EST 20-MAY-2001
LOCUS SEAMC007944 Sea urchin primary mesenchyme cell cDNA library
DEFINITION Strongylocentrotus purpuratus cDNA clone PM990802-04-0459 5', mRNA
sequence.
ACCESSION BG787987
VERSION BG787987.1 GI:14159000
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 818)
Zhu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. and
Ettensohn, C.A.
A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo
Development 128 (13), 2615-2627 (2001)
21384984
PUBMED 11493577
Contact: Ettensohn CA
Dept. Biol. Sci.
Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh, PA 15213, USA
Tel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
Location/Qualifiers
1. 818
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="PM990802-04-0459"
/tissue_type="embryo"
/cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea urchin primary mesenchyme cell cDNA
library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; oligo
at priming from poly A+ RNA, directionally cloned"

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ORIGIN

```

Query Match      82.4%; Score 34.6; DB 4; Length 818;
Best Local Similarity 90.2%; Pred. No. 5.8;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGGAAGGGGGAAGGGAAGGAGTGAAGCGAGGAGCTGAA 41
    |||||
Db 655 AGCGAAGGGGGAAGGGAAGGAGTGAAGCGAGGAGCTGAA 695
    |||||

```

RESULT 5	AZ649302/c
LOCUS	AZ649302.1
DEFINITION	Mus musculus genomic clone UGUC1M051&F16 R, genomic survey sequence.
ACCESSION	AZ649302
VERSION	AZ649302.1
KEYWORDS	GI:11782476
SOURCE	GSS:
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 643)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.,
TITLE	Mus whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss

94112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0518 row: F column: 16
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence ston: 643

```

FEATURES
source
    Location/Qualifiers
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0518P16"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (Gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adapted mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

```

	Query Match	78.8%	Score 33;	DB 8;	Length 643;
	Best Local Similarity	87.8%	Pred. No. 16;		
	Matches 36;	Conservative	0;	Mismatches 5;	Indels 0;
	Gaps	0;			
QY	2	AGGAAGCGAGGGAAGCGGAGGTGAAGGAGGTGAAA	42		
Db	104	AGGATCGAGGTAAAGGAGGAGGGAAGGAAGGAGGTGAGA	64		

RESULT	6
A1252833	
LOCUS	103 bp mRNA linear EST 05-NOV-1998 qV49f02.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1984923 3'
DEFINITION	mRNA sequence.
ACCESSION	A1252833
VERSION	A1252833
KEYWORDS	EST.
SOURCE	A1252833.1 GI:3849362
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 103) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE	Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapsb@mail.nih.gov
COMMENT	unknown library type Seq primer: -40UP from Gibco.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1984923"
/sex="female"
/tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov32"
/note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 500 bp. Non-amplified library."

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[illegible]

RESULT 7	AZ022385	154 bp	DNA	linear	GSS 25-FEB-2000
LOCUS	RPCI-23-385H23.TV	RPCI-23	Mus musculus	genomic clone	
DEFINITION	RPCI-23-385H23, genomic survey sequence.				
ACCESSION	AZ022385				
VERSION	AZ022385.1	GI:7097769			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 154)				
AUTHORS	Zhao, S., Niernan, W., Feldblyum, T., Malek, J., Shatsman, S.,				
	Akinret, B., Levine, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de				
	Jong, P. and Fraser, C.M.				

RESULT 11

Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 1154199]]. EG cells were obtained from Dr. Brigid L.M. Hogan and RNA was prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells were cultured at 37 °C, 5% CO₂ in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 2 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10⁻⁷ units of LiF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer ([Invitrogen: 5'-pGACTAGTTCTACATCGACGGCCGCCTTTTTTTTTT-3']) from 2.5 µg of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr. Kazuhiro Kondo at AISIS Cosmos. Then the subtracted cDNAs were cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo."

ORIGIN

	Query Match	74.8%;	Score 31.4;	DB 7;	Length 524;
	Best Local Similarity	85.4%;	Pred. No. 45;		
	Matches	35;	Conservative	0;	Mismatches 6; Indels 0; Gaps 0;
Qy	1	AAGGAAGGAGGGAGAAGGAGGAGGTCAAGGAAGGAGTGAA	41		
Dd	447	AAGGAAGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGA	407		

Search completed: March 13, 2005, 18:14:03
Job time : 144.39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 12:28:28 ; Search time 478.866 Seconds
(without alignments)
8757.724 Million cell updates/sec

Title: US-09-617-720A-1
Perfect score: 2563
Sequence: 1 agggaggtctacacctgtg.....ataatatcgagagaagaga 2563

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/prodata/1/ina/5B COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUS COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2515.2	98.1	2699	4	US-09-949-016-3485
2	2488.4	97.1	2648	3	US-09-417-455-6
3	2488.4	97.1	2648	3	US-09-348-942-6
4	2488.4	97.1	2648	3	US-09-457-626-6
5	2488.4	97.1	2648	4	US-09-576-008-6
6	2488.4	97.1	2720	4	US-09-949-016-956
7	2245.2	87.6	9634	4	US-09-949-016-12698
8	2245.2	87.6	9641	4	US-09-949-016-15227
9	2220.4	86.6	7605	3	US-09-417-455-8
10	2220.4	86.6	7605	3	US-09-348-942-8
11	2220.4	86.6	7605	3	US-09-457-626-8
12	2220.4	86.6	7605	4	US-09-576-008-8
13	1616.6	63.1	5751	3	US-09-417-455-7
14	1616.6	63.1	5751	3	US-09-348-942-7
15	1616.6	63.1	5751	3	US-09-457-626-7
16	1616.6	63.1	5751	4	US-09-576-008-7
17	1195.2	46.6	1282	3	US-09-417-455-4
18	1195.2	46.6	1282	3	US-09-348-942-4
19	1195.2	46.6	1282	3	US-09-457-626-4
20	1195.2	46.6	1282	4	US-09-576-008-4
21	941.2	36.7	985	3	US-09-417-455-2
22	941.2	36.7	985	3	US-09-348-942-2
23	941.2	36.7	985	3	US-09-457-626-2
24	941.2	36.7	985	4	US-09-576-008-2
25	600.6	23.4	601	4	US-09-949-016-36664
26	600.6	23.4	601	4	US-09-949-016-123784
27	285	11.1	357	3	US-09-417-455-1

28	285	11.1	357	3	US-09-348-942-1	Sequence 1, Appli	
29	285	11.1	357	3	US-09-457-626-1	Sequence 1, Appli	
30	285	11.1	357	4	US-09-576-008-1	Sequence 1, Appli	
31	198.6	7.7	466	4	US-09-573-080A-102	Sequence 102, App	
C	32	155.8	6.1	374159	4	US-09-949-016-15868	Sequence 15868, A
	33	153.2	6.0	100550	4	US-09-949-016-11835	Sequence 11835, A
	34	153.2	6.0	100551	4	US-09-949-016-16207	Sequence 16207, A
	35	149.2	5.8	95750	4	US-09-949-016-11926	Sequence 11926, A
C	36	149.2	5.8	213456	4	US-09-820-007-3	Sequence 3, Appli
	37	149.2	5.8	323820	4	US-09-949-016-14139	Sequence 14139, A
	38	148.4	5.8	231129	4	US-09-949-016-16110	Sequence 16110, A
39	148.4	5.8	266293	4	US-09-949-016-11934	Sequence 11934, A	
40	145.4	5.7	124480	4	US-09-949-016-15921	Sequence 15921, A	
C	41	139.2	5.4	64046	4	US-09-949-016-12560	Sequence 12560, A
	42	139.2	5.4	64047	4	US-09-949-016-15781	Sequence 15781, A
C	43	139	5.4	60417	4	US-09-949-016-13312	Sequence 13312, A
C	44	138.8	5.4	390890	4	US-09-949-016-14720	Sequence 14720, A
	45	138.6	5.4	108310	4	US-09-949-016-16366	Sequence 16366, A

ALIGNMENTS

RESULT 1

US-09-949-016-3485

; Sequence 3485, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3485

; LENGTH: 2699

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-3485

Query Match 98.1%; Score 2515.2; DB 4; Length 2699;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2553; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

QY 1 AGGGAGTCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGTGCTTCGAA 60

DB 133 AGGGAGTCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGTGCTTCGAA 192

QY 61 TGAAGGACTCGGCATTGAAGGTCTTTATCTGCATAATAACCACTTCTAGCTGGAGGC 120

DB 193 TGAAGGACTCGGCATTGAAGGTCTTTATCTGCATAATAACCACTTCTAGCTGGAGGC 252

QY 121 TGCATGACGGGAAGGTCAATTAAGGTGAAGAGATCAAGCGTGGTCCCAATCGGTGGCTGG 180

DB 253 TGCATGACGGGAAGGTCAATTAAGGTGAAGAGATCAAGCGTGGTCCCAATCGGTGGCTGG 312

QY 181 ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGTTGGAAGCCAGTGCCTCTCATGTG 240

DB 313 ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGTTGGAAGCCAGTGCCTCTCATGTG 372

QY 241 GGGTGGGAGAGAGCGGCTCTTAACACTAGAGCCAGTGAACATCATGGAGCTTACTTCTG 300

DB 373 GGGTGGGAGAGAGCGGCTCTTAACACTAGAGCCAGTGAACATCATGGAGCTTACTTCTG 432

QY 301 GTGCCAAGGAATCCAAAGAGCTTTCACCTTCTACCGGGGGGACATGGGGCTCACCTCCAGCT 360

Db 433 GTGCCAAGAAATCCAGAGCTTACCTTCTACGGCGGACATGGGGCTCACCTCCAGCT 492
QY 361 TCGAGTCGGCTGCTACCCGGGTGGTTCCTGTGCACGGTGCTGAAGCCGATCAGCCTG 420
Db 493 TCGAGTCGGCTGCTACCCGGGTGGTTCCTGTGCACGGTGCTGAAGCCGATCAGCCTG 552
QY 421 TCAGACTCACCCAGCTTCCCGAAGATGGTGGTGGAAATGCCCCCATCAAGACTTCTACT 480
Db 553 TCAGACTCACCCAGCTTCCCGAAGATGGTGGTGGAAATGCCCCCATCAAGACTTCTACT 612
QY 481 TCCAGCAGTGTGACTAGGGCAACGTGCCCGCCCGAGAACTCCCTGGGCGAGAGCCAGCTGG 540
Db 613 TCCAGCAGTGTGACTAGGGCAACGTG-CGCCCGAGAACTCCCTGGGCGAGAGCCAGCTGG 671
QY 541 GTGAGGGGTGAGTGAGGAGAGCCATGGCGGACAACTCTCTTCTGTGTTCCAGTTTCATATAATT 600
Db 672 GTGAGGGGTGAGTGAGGAGAGCCATGGCGGACAACTCTCTCTGTCTCTCAGGACCC 731
QY 601 CAGGTCTGACTTGTGGGCACTGACCACTTGTCTTCTGTGTTCCAGTTTCATATAATT 660
Db 732 CAGGTCTGACTTGTGGGCACTGACCACTTGTCTTCTGTGTTCCAGTTTCATATAATT 791
QY 661 CTGAGATTGGAGCTCAGTCCAGGTCCTCCCGCACTGGATGGTCTACTGTGTGGAAC 720
Db 792 CTGAGATTGGAGCTCAGTCCAGGTCCTCCCGCACTGGATGGTCTACTGTGTGGAAC 851
QY 721 CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAAGAATTTCTGTGGGGTGG 780
Db 852 CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAAGAATTTCTGTGGGGTGG 911
QY 781 GTGGGGAGTGTGGGAATCAATTCCTGTCTTAATGTGAATGACAAAGTTTACCTTGAGCC 840
Db 912 GTGGGGAGTGTGGGAATCAATTCCTGTCTTAATGTGAATGACAAAGTTTACCTTGAGCC 971
QY 841 CGCAGGCCAACCCATCCCACTGAGCTTATAGGCTTATAGGCTCAGTAGCTCTCCAATGAAGTC 900
Db 972 CGCAGGCCAACCCATCCCACTGAGCTTATAGGCTTATAGGCTCAGTAGCTCTCCAATGAAGTC 1031
QY 901 CTCTCACTCACCACCTGTGCAGAGAGGGAGGTGCTCATAGCTCAGGATCTATGGCCCT 960
Db 1032 CTGTCACTCACCACCTGTGCAGAGAGGGAGGTGCTCATAGCTCAGGATCTATGGCCCT 1091
QY 961 TGGCCAGGCCCAACCCCTTCCCTTT-ATCCTGCCACTGCTCATATGCTACCTTTCTATC 1019
Db 1092 TGGCCAGGCCCAACCCCTTCCCTTTAACTCCTGCCACTGTCTATGCTACCTTTCTATC 1151
QY 1020 TCTTCCCTCATCTTGTGTGGGATGAGAGGTGGTGTGATGTCAGAAAGAAATGGTTGG 1079
Db 1152 TCTTCCCTCATCTTGTGTGGGATGAGAGGTGGTGTGATGTCAGAAAGAAATGGTTGG 1211
QY 1080 AGCTCAGAGATAAAGATAAGTAGGTATGCTATGCTCTTTTAAAGAACCCAGATACA 1139
Db 1212 AGCTCAGAGATAAAGATAAGTAGGTATGCTATGCTCTTTTAAAGAACCCAGATACA 1271
QY 1140 ATCAAAATCCAGAGTCTGGTCTCTATTCCTCATGAAAAGTGTCTCATGACATATTGAGAA 1199
Db 1272 ATCAAAATCCAGAGTCTGGTCTCTATTCCTCATGAAAAGTGTCTCATGACATATTGAGAA 1331
QY 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTTATA 1259
Db 1332 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTTATA 1391
QY 1260 TATTTCTTTATAGAAAAGTCTGAGAGTTTACTTCAATTTAGACATGTCAGGTTGG 1319
Db 1392 TATTTCTTTATAGAAAAGTCTGAGAGTTTACTTCAATTTAGACATGTCAGGTTGG 1451
QY 1320 TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAAATTTTC 1379
Db 1452 TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAAATTTTC 1511
QY 1380 TACAATGAAGATGAATTCCTTGATAAAAAATGAAGAAATTAATCTGTGAGGTAAGCA 1439

Db 1512 TACAATGAAGATGAATTCCTTGATAAAAAATGAAGAAAGAAATTAATCTTGAGGTAAGCA 1571
QY 1440 GAGCAGACATCATCTCTGATTGCTCAGCCTCCAAATTCCTCCAGAGTAAATTCAAATTGA 1499
Db 1572 GAGCAGACATCATCTCTGATTGCTCAGCCTCCAAATTCCTCCAGAGTAAATTCAAATTGA 1631
QY 1500 ATCGAGCTCTGCTGCTCTGCTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1559
Db 1632 ATCGAGCTCTGCTGCTCTGCTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1691
QY 1560 CACTCAGAGAGGAGCTGCTCAGTTTGTGGCTGGAACTCTCTGGTAAGGAACTTAAA 1619
Db 1692 CACTCAGAGAGGAGCTGCTCAGTTTGTGGCTGGAACTCTCTGGTAAGGAACTTAAA 1751
QY 1620 GAACAAAAATCATCTGTAATTTCTTCTAGAAAGATCACAGCCCTCGGATTCAGAGC 1679
Db 1752 GAACAAAAATCATCTGTAATTTCTTCTAGAAAGATCACAGCCCTCGGATTCAGAGC 1811
QY 1680 ATTGATCCAGTCTCTAAGAGGCTGTACTGTGTTGAATTTGTGCCCTTCAAATTCA 1739
Db 1812 ATTGATCCAGTCTCTAAGAGGCTGTACTGTGTTGAATTTGTGCCCTTCAAATTCA 1871
QY 1740 CATCTCTTCTGGAATCTCAGTCTGAGTTTATTTGGAGATAAGCTCTCTGCAGATGTAG 1799
Db 1872 CATCTCTTCTGGAATCTCAGTCTGAGTTTATTTGGAGATAAGCTCTCTGCAGATGTAG 1931
QY 1800 TTAGTTAAAGACAAGGTCTGCTGATGAAGGTAGACCTAAATTTCAATATGACTGTTTCC 1859
Db 1932 TTAGTTAAAGACAAGGTCTGCTGATGAAGGTAGACCTAAATTTCAATATGACTGTTTCC 1991
QY 1860 TTGTATGAAAAGGAGAGACACAGAGACAGAGGAGACGCGGGGAAAGACTATGTAAGATG 1919
Db 1992 TTGTATGAAAAGGAGAGACACAGAGACAGAGGAGACGCGGGGAAAGACTATGTAAGATG 2051
QY 1920 AAGCAGAGATCGGAGTTTTCGAGCCACAAGCTAAGAAACACCAAGGATTTGGCAACCA 1979
Db 2052 AAGCAGAGATCGGAGTTTTCGAGCCACAAGCTAAGAAACACCAAGGATTTGGCAACCA 2111
QY 1980 TCAGAAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGCG 2039
Db 2112 TCAGAAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGCG 2171
QY 2040 TCTGCTGAAAACCTTAATCTCAGACTTCCAGCTCTCTGAAACGAAAGAAATTAATTTCCG 2099
Db 2172 TCTGCTGAAAACCTTAATCTCAGACTTCCAGCTCTCTGAAACGAAAGAAATTAATTTCCG 2231
QY 2100 CTGTTTAAAGCCCAAGGATTAATTTGTTTACAGAGCTCTAGGAACTTAATACAGCTCT 2159
Db 2232 CTGTTTAAAGCCCAAGGATTAATTTGTTTACAGAGCTCTAGGAACTTAATACAGCTCT 2291
QY 2160 AAAATGATCCCTGTCTCTCGTGTGTTTACATTTCTGTGTGTGCTCCCTCCCAATGTACCA 2219
Db 2292 AAAATGATCCCTGTCTCTCGTGTGTTTACATTTCTGTGTGTGCTCCCTCCCAATGTACCA 2351
QY 2220 AAGTTGCTTTGTGACCAATAGAAATATGGCAGAAAGTGTGTCATGCCATTTCCAGATT 2279
Db 2352 AAGTTGCTTTGTGACCAATAGAAATATGGCAGAAAGTGTGTCATGCCATTTCCAGATT 2410
QY 2280 AGGTTATAAAGACACTGAGCTTCTACTTGGCCCTCTCTCTGCGCAACCCACCGCC 2339
Db 2411 AGGTTATAAAGACACTGAGCTTCTACTTGGCCCTCTCTCTGCGCAACCCACCGCC 2470
QY 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCAGGCTTA 2399
Db 2471 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCAGGCTTA 2530
QY 2400 TAAAGAGACTTACGTGGTAAATAAATGAAGTCTCTGCCCAAGCAACCAATAGTAACTTA 2459
Db 2531 TAAAGAGACTTACGTGGTAAATAAATGAAGTCTCTGCCCAAGCAACCAATAGTAACTTA 2590
QY 2460 GAGCAGAGACTCTGTGAGATAATCGATTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519
Db 2591 GAGCAGAGACTCTGTGAGATAATCGATTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2650

Db 453 TCAGACTCACCAGCTTCCGAGAATGGTGGCTGGAATGCCCCATCAGACTTCTACT 512
Qy 481 TCAGCAGTGTGACTAGGCAAGCTGCCCCGAGAACTCCCTGGGCAAGCCAGCTCGG 540
Db 513 TCAGCAGTGTGACTAGGCAAGCTG - CCCCCAGAACTCCCTGGGCAAGCCAGCTCGG 571
Qy 541 GTGAGGGGTGAGTGGAGGAGCCATGGCGGCAATCACTCTTCTGCTCTCAGGACCCC 600
Db 572 GTGAGGGGTGAGTGGAGGAGCCATGGCGGCAATCACTCTCTGCTCTCAGGACCCC 631
Qy 601 CAGGCTGACTTGTGGGCACTGACCACTTGTGTCTTCTGTTCCAGTTCGATATAATT 660
Db 632 CAGCTGACTTGTGGGCACTGACCACTTGTGTCTTCTGTTCCAGTTCGATAAATT 691
Qy 661 CTGAGATTGGAGCTCAGTCCAGGTCCTCCGCCACTGGATGGTCTACTGCTGGGAAC 720
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Qy 721 CTTGTAAAAACCATGTGGGGTAACTGGGAAATAACAATGAAGAATTTCTGTGGGGTGGG 780
Db 752 CTTGTAAAAACCATGTGGGGTAACTGGGAAATAACAATGAAGAATTTCTGTGGGGTGGG 811
Qy 781 GTGGGGGAGTGTGGGAATCATTTCTGCTTAATGGTAACTGCAAGTGTACCTCGAGCC 840
Db 812 GTGGGGGAGTGTGGGAATCATTTCTGCTTAATGGTAACTGCAAGTGTACCTCGAGCC 871
Qy 841 CCGCAGGCCAAACCATCCCGAGTTGAGCCTTAATAGGGTCAGTAGCTCTCCAATGAAGTC 900
Db 872 CCGCAGGCCAAACCATCCCGAGTTGAGCCTTAATAGGGTCAGTAGCTCTCCAATGAAGTC 931
Qy 901 CTCCTCACTCACCACCTGTGCAGAGAGGAGGTGTCATAGACTCAGGATCTATGGCCCT 960
Db 932 CTGTCACTCACCACCTGTGCAGAGAGGAGGTGTCATAGACTCAGGATCTATGGCCCT 991
Qy 961 TGGCCCGAGCCCAACCCCTTCCCTTT - ATCTGCGCACTGTCATATGCTACCTTTCTATC 1019
Db 992 TGGCCCGAGCCCAACCCCTTCCCTTTAATCTTCCACTGTCAATGCTACCTTTCTATC 1051
Qy 1020 TCTTCCCTCATCATTTGTGTGGGCATGAGAGGTGGTGTGTCAGAGAATAAGTTGCG 1079
Db 1052 TCTTCCCTCATCATTTGTGTGGGCATGAGAGGTGGTGTGTCAGAGAATAAGTTGCG 1111
Qy 1080 AGCTCAGAGATAAAGATAGTAGGATGCTGATCCTCTTTTAAACCACCAAGATACA 1139
Db 1112 AGCTCAGAGATAAAGATAGTAGGATGCTGATCCTCTTTTAAACCACCAAGATACA 1171
Qy 1140 ATCAAAATCCAGATGCTGCTTATTCCTATGAAAAGTCTCATGACATATTGAGAA 1199
Db 1172 ATCAAAATCCAGATGCTGCTTATTCCTATGAAAAGTCTCATGACATATTGAGAA 1231
Qy 1200 GACCTACTTACAAAGTGGCATATA - TTGCAATTTATTTTAAATAAAGATACCTATTAT 1258
Db 1232 GACCTACTTACAAAGTGGCATATAATTGCAATTAATTTTAAATAAAGATACCTATTAT 1291
Qy 1259 ATATTTCTTTATAGAAAAAGTCTGGAAGTTTACTTCAATTTAGCAATGTCCAGGGTG 1318
Db 1292 ATATTTCTTTATAGAAAAAGTCTGGAAGTTTACTTCAATTTAGCAATGTCCAGGGTG 1351
Qy 1319 GTGGCAGTATAGTTCATTTTCTTTTAAATTCGTAAATTTATCTGATTTCTTAATTTT 1378
Db 1352 GTGGCAGTATAGTTCATTTTCTTTTAAATTCGTAAATTTATCTGATTTCTTAATTTT 1411
Qy 1379 CTACAATGAAGATGAATTTCTTTGTATAAAAAATAAGAAAGAAATTAATCTTGAGTAAGC 1438
Db 1412 CTACAATGAAGATGAATTTCTTTGTATAAAAAATAAGAAAGAAATTAATCTTGAGTAAGC 1471
Qy 1439 AGAGCAGACATCATCTCTGATGTCCTCGCCCTCAATTTCCCGAGTAATTTCAAAATTG 1498
Db 1472 AGAGCAGACATCATCTCTGATGTCCTCAGCCCTCACTTTCCCGAGTAATTTCAAAATTG 1531
Qy 1499 AATCGAGCTCTGCTGCTGTTGTTGTGTAGTAGTATCAGGAAACAGATCTCAGCAAG 1558
Db 1532 AATCGAGCTCTGCTGCTGTTGTTGTGTAGTAGTATCAGGAAACAGATCTCAGCAAG 1591

RESULT 4
US-09-457-626-6
; Sequence 6, Application US/09457626

Qy 1559 CCACTGAGGAGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA 1618
Db 1592 CCACTGAGGAGGAGGCTGTGCTGAAGTTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA 1651
Qy 1619 AGAAACAAAATCATCTGGTAAATTTCTTCTAGAAAGATCACAGCCCTCTGGGATTTCCAAGG 1678
Db 1652 AGAAACAAAATCATCTGGTAAATTTCTTCTAGAAAGATCACAGCCCTCTGGGATTTCCAAGG 1711
Qy 1679 CAATGGATCCAGTCTCTAAAGAGGCTGTGTACTGTGTTGAAATTTGTCTCCCTCAAAATTC 1738
Db 1712 CAATGGATCCAGTCTCTAAAGAGGCTGTGTACTGTGTTGAAATTTGTCTCCCTCAAAATTC 1771
Qy 1739 ACATCTCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTTGGAGATAAGGTCTCTGCAGATGTA 1798
Db 1772 ACATCTCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTTGGAGATAAGGTCTCTGCAGATGTA 1831
Qy 1799 GTTAGTTAAGACAAGTCTCATGCTGGATGAAGGTAGACCTTAAATTTCAATATGACTGGTTTC 1858
Db 1832 GTTAGTTAAGACAAGTCTCATGCTGGATGAAGGTAGACCTTAAATTTCAATATGACTGGTTTC 1891
Qy 1859 CTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGAAGACCTATGTAAGAT 1918
Db 1892 CTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGAAGACCTATGTAAGAT 1951
Qy 1919 GAAGGACAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTTGTGGCAACC 1978
Db 1952 GAAGGACAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTTGTGGCAACC 2011
Qy 1979 ATCAGAAGCTTGGAGAGGCAAGAGATTTCTTCCCTAGAGGCTTTAGAGGATTAACGG 2038
Db 2012 ATCAGAAGCTTGGAGAGGCAAGAGATTTCTTCCCTAGAGGCTTTAGAGGATTAACGG 2071
Qy 2039 CTCTGCTGAAACCTTAAATCTCAGACTTCAGGCTCTCTGAAACGAAGAAATAAATTTTCG 2098
Db 2072 CTCTGCTGAAACCTTAAATCTCAGACTTCAGGCTCTCTGAAACGAAGAAATAAATTTTCG 2131
Qy 2099 GCTGTTTTAAGCCACAAGGATAATTGGTTACAGAGCTCTAGGAACTTAATACAGCTGC 2158
Db 2132 GCTGTTTTAAGCCACAAGGATAATTGGTTACAGAGCTCTAGGAACTTAATACAGCTGC 2191
Qy 2159 TAAATGATCCCTGCTCTCTGCTGTTTACATTTCTGTGTGTGCTCCCTCCCAACATGTACC 2218
Db 2192 TAAATGATCCCTGCTCTCTGCTGTTTACATTTCTGTGTGTGCTCCCTCCCAACATGTACC 2251
Qy 2219 AAAAGTTGCTTTGTGACCCCAATAGATAATGGCAGAAAGTATGGCATGCCACTTCCAAAGAT 2278
Db 2252 AAAAGTTGCTTTGTGA - CCAATAGAAATATGGCAGAAAGTATGGCATGCCACTTCCAAAGAT 2310
Qy 2279 TAGGTTATAAAGACACATGCGAGCTTCTACTTGAAGCCCTCTCTCTGCGACCCACCGCCC 2338
Db 2311 TAGGTTATAAAGACACATGCGAGCTTCTACTTGAAGCCCTCTCTCTGCGACCCACCGCCC 2370
Qy 2339 CCAATCTATCTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCGCATGCTATGAGCAGGCT 2398
Db 2371 CCAATCTATCTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCGCATGCTATGAGCAGGCT 2430
Qy 2399 ATAAAGAGACTTACCTGGTAAATAAATGAAGTCTCTGCCACAGCAGCACATTAAGTAACT 2458
Db 2431 ATAAAGAGACTTACCTGGTAAATAAATGAAGTCTCTGCCACAGCAGCACATTAAGTAACT 2490
Qy 2459 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTT - AAGTTGCTCAGTTTTGCT 2517
Db 2491 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTT - AAGTTGCTCAGTTTTGCT 2550
Qy 2518 CTAACCTTGTATGACGCAATAGATAAATAATATGACAGAGAAAGAGA 2563
Db 2551 CTAACCTTGTATGACGCAATAGATAAATAATATGACAGAGAAAGAGA 2596

QY 1559 CCACTGAGGAGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA 1618
Db 1592 CCACCTGAGGAGAGGCTGTGCTGAAATTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA 1651
QY 1619 AGAACAAAATCATCTGGTAAATCTTTCTAGAGGATCACAGCCCTCGGATTCGAAG 1678
Db 1652 AGAACAAAATCATCTGGTAAATCTTTCTAGAGGATCACAGCCCTCGGATTCGAAG 1711
QY 1679 CAATGGATCCAGTCTCTAAGAGGCTGTGTAATCTGGTTGAATGTGTCCTCCCTCAAAATTC 1738
Db 1712 CAATGGATCCAGTCTCTAAGAGGCTGTGTAATCTGGTTGAATGTGTCCTCCCTCAAAATTC 1771
QY 1739 ACATCCTCTCTGGATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGA 1798
Db 1772 ACATCCTCTCTGGATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGA 1831
QY 1799 GTTAGTTAAGACAAGTCTAGTCTGATGAAGGTAGACCTTAAATCTCAATATGCTGTTTC 1858
Db 1832 GTTAGTTAAGACAAGTCTAGTCTGATGAAGGTAGACCTTAAATCTCAATATGCTGTTTC 1891
QY 1859 CTTGTATGAAAAGAGAGGACACAGAGACAGAGGAGACCGGGGAAGACTATGTAAAGAT 1918
Db 1892 CTTGTATGAAAAGAGAGGACACAGAGACAGAGGAGACCGGGGAAGACTATGTAAAGAT 1951
QY 1919 GAAGCAGAGATCGAGATTTTCAGGCCACAAGCTAAGAAACACCAAGGATTTGTGCAACC 1978
Db 1952 GAAGCAGAGATCGAGATTTTCAGGCCACAAGCTAAGAAACACCAAGGATTTGTGCAACC 2011
QY 1979 ATCAGAAGCTTGAAGAGGCAAGAGATTTCTCCCTAGAGGCTTTAGAGGATAACGG 2038
Db 2012 ATCAGAAGCTTGAAGAGGCAAGAGATTTCTCCCTAGAGGCTTTAGAGGATAACGG 2071
QY 2039 CTTCTCTGAAACCTTAAATCTCAGACTTCAGGCTCTCTGAGGCTCTCTGAAAGAAATAAATTTTCG 2098
Db 2072 CTTCTCTGAAACCTTAAATCTCAGACTTCAGGCTCTCTGAGGCTCTCTGAAAGAAATAAATTTTCG 2131
QY 2099 GCTGTTTTAAGCCACAAGGATAATTTGTTACAGAGCTCTAGGAAACTAATACAGCTGC 2158
Db 2132 GCTGTTTTAAGCCACAAGGATAATTTGTTACAGAGCTCTAGGAAACTAATACAGCTGC 2191
QY 2159 TAAATATGATCCCTGTCTCTCTGTTTACATTTCTGTGTGTGTCCTCCCTCCCAATGTACC 2218
Db 2192 TAAATATGATCCCTGTCTCTCTGTTTACATTTCTGTGTGTGTCCTCCCTCCCAATGTACC 2251
QY 2219 AAAAGTTGTCTTTGTGACCCCAATAGAAATATGGCAGAGTATGGCATTCGCAAGAT 2278
Db 2252 AAAAGTTGTCTTTGTGAC - CCAATAGAAATATGGCAGAGTATGGCATTCGCAAGAT 2310
QY 2279 TAGGTTATAAAGACACTGACGCTTCTACTTGGCCCTCTCTCTGACCCACCCGCGCC 2338
Db 2311 TAGGTTATAAAGACACTGACGCTTCTACTTGGCCCTCTCTCTGACCCACCCGCGCC 2370
QY 2339 CCAATCTATCTTGGCTCACTCGCTCTGGGGAGGCTAGTGCATGCTATGAGCAGGCT 2398
Db 2371 CCAATCTATCTTGGCTCACTCGCTCTGGGGAGGCTAGTGCATGCTATGAGCAGGCT 2430
QY 2399 ATAAAGAGACTTACCTGGTAAAAATGAAGTCTCTGCCCCCAGCCACATTAAGTGAACCT 2458
Db 2431 ATAAAGAGACTTACCTGGTAAAAATGAAGTCTCTGCCCCCAGCCACATTAAGTGAACCT 2490
QY 2459 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTT - AAGTTGCTCAGTTTGGT 2517
Db 2491 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTTAAAGTTGCTCAGTTTGGT 2550
QY 2518 CTAACCTGTTATGACCAATAGATAAATAATATGACAGAAAGAGA 2563
Db 2551 CTAACCTGTTATGACCAATAGATAAATAATATGACAGAAAGAGA 2596

RESULT 5

US-09-576-008-6
; Sequence 6, Application US/09576008
; Patent No. 6541623

GENERAL INFORMATION:

; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-Yue
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US/09/576,008
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2648
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-576-008-6

Query Match 97.1%; Score 2488.4; DB 4; Length 2648;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY 1 AGGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTGCTTCGAA 60
Db 33 AGGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTGCTTCGAA 92
QY 61 TGAAGGACTCGGCATTGAAGGTGCTTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 120
Db 93 TGAAGGACTCGGCATTGAAGGTGCTTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 152
QY 121 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCCAATCGGTGGCTGG 180
Db 153 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCCAATCGGTGGCTGG 212
QY 181 ATGCCAGCTGTCCCCCGTCATCTGGGTGTCAGGTTGGAAGCCAGCTGCTCATGTG 240
Db 213 ATGCCAGCTGTCCCCCGTCATCTGGGTGTCAGGTTGGAAGCCAGCTGCTCATGTG 272
QY 241 GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
Db 273 GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 332
QY 301 GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGCGGGACATGGGGCTCACTCCAGCT 360
Db 333 GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGCGGGACATGGGGCTCACTCCAGCT 392
QY 361 TCGAGTGGCTGCTTACCGGGCTGTTCTCTGTGACCGTGTGCTGAAGCCGATCAGCTG 420
Db 393 TCGAGTGGCTGCTTACCGGGCTGTTCTCTGTGACCGTGTGCTGAAGCCGATCAGCTG 452

RESULT 6
US-09-949-016-956
; Sequence 956, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 956
; LENGTH: 2720
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-956

Query Match 97.1%; Score 2488.4; DB 4; Length 2720;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY	1	AGGGAGTCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGGCGTGTCTCCGAA	60
DB	134	AGGGAGTCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGGCGTGTCTCCGAA	193
QY	61	TGAAGGACTCGGCATGAAGTGTCTTATCTGCATAAACCAGCTTCTAGCTGAGGCG	120
DB	194	TGAAGGACTCGGCATGAAGTGTCTTATCTGCATAAACCAGCTTCTAGCTGAGGCG	253
QY	121	TGCATGACGGAAGTCAATTAAGTGAAGAGATCAGCGTGTGCCAATCGTGGCTGG	180
DB	254	TGCATGACGGAAGTCAATTAAGTGAAGAGATCAGCGTGTGCCAATCGTGGCTGG	313
QY	181	ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGCTGGAAGCCAGTGCCTCATGTG	240
DB	314	ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGCTGGAAGCCAGTGCCTCATGTG	373
QY	241	GGGTGGGCGAGGCGGACTCTAACACTAGACCAAGTGAACATCATGAGCTCTATCTTG	300
DB	374	GGGTGGGCGAGGCGGACTCTAACACTAGACCAAGTGAACATCATGAGCTCTATCTTG	433
QY	301	GTGCCAAGGAATCCAAGAGCTTCACTTTCTACCGCGGGACATGGGGCTCACCTCCAGCT	360
DB	434	GTGCCAAGGAATCCAAGAGCTTCACTTTCTACCGCGGGACATGGGGCTCACCTCCAGCT	493
QY	361	TGAGTCCGCTGCTTACCGGGCTGTTCTGTGTCACCGTGTGCAAGCCGATCAGCCTG	420
DB	494	TGAGTCCGCTGCTTACCGGGCTGTTCTGTGTCACCGTGTGCAAGCCGATCAGCCTG	553
QY	421	TCAGACTCACCCAGCTTCCCGAAGATGGTGGCTGGAATGCCCGCATCAGACTTCTACT	480
DB	554	TCAGACTCACCCAGCTTCCCGAAGATGGTGGCTGGAATGCCCGCATCAGACTTCTACT	613
QY	481	TCCAGCAGTGTGACTAGGGCAACGTCGCCCGCCAGAACTCCCTGGGCGAGCCAGCTCGG	540
DB	614	TCCAGCAGTGTGACTAGGGCAACGTCGCCCGCCAGAACTCCCTGGGCGAGCCAGCTCGG	672
QY	541	GTGAGGGTGTAGTGAGAGACCCATGGCGGCAATCACTCTTTCTGTCTCAGAGCCCG	600
DB	673	GTGAGGGTGTAGTGAGAGACCCATGGCGGCAATCACTCTCTGTCTCAGAGCCCG	732
QY	601	CAGGCTCAGCTTGTAGGGGCACTGACCTTGTCTCTGTGTTCCAGTTTGCATAAATT	660
DB	733	CAGGCTCAGCTTGTAGGGGCACTGACCTTGTCTCTGTGTTCCAGTTTGCATAAATT	792

QY	661	CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCCCACTGGATGGTCTACTGCTGTGAAC	720
DB	793	CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCCCACTGGATGGTCTACTGCTGTGAAC	852
QY	721	CTTTGAAAAACCATGTGGGTAAACTGGGAATAACATGAAAAATTTCTGTGGGGTGGG	780
DB	853	CTTTGAAAAACCATGTGGGTAAACTGGGAATAACATGAAAAATTTCTGTGGGGTGGG	912
QY	781	GTGGGGAGTGTGGGAATCAATCTCTGCTTAATGTGTAACAAAGTGTACCTGAGCC	840
DB	913	GTGGGGAGTGTGGGAATCAATCTCTGCTTAATGTGTAACAAAGTGTACCTGAGCC	972
QY	841	CGCAGGCGCAACCCATCCCGAGTTGAGCCTTATAGGGTCAGTCTCCCATGAAGTC	900
DB	973	CGCAGGCGCAACCCATCCCGAGTTGAGCCTTATAGGGTCAGTCTCCCATGAAGTC	1032
QY	901	CTCTCACTCACCACCTGTGCAGGAGAGGGGTGGTCAATAGAGTCAGGGATCTATGGCCCT	960
DB	1033	CTGTCACTCACCACCTGTGCAGGAGAGGGGTGGTCAATAGAGTCAGGGATCTATGGCCCT	1092
QY	961	TGGCCAGCCCGCCCTTCCCTTTT-ATCTGCGCACTGTCTCATATGCTACCTTTCTATC	1019
DB	1093	TGGCCAGCCCGCCCTTCCCTTTTAACTCTGCGCACTGTCTCATATGCTACCTTTCTATC	1152
QY	1020	TCTTCCCTCATCATCTTGTGTGGCATGAGAGGTGTGTGATGTCAAGAATAATGTTG	1079
DB	1153	TCTTCCCTCATCATCTTGTGTGGCATGAGAGGTGTGTGATGTCAAGAATAATGTTG	1212
QY	1080	AGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTTAAAAACCCAAAGATCA	1139
DB	1213	AGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTTAAAAACCCAAAGATCA	1272
QY	1140	ATCAAAATCCAGATGTGCTCTTATTTCCCATGAAAAAGTCTCATGATATTTGAGAA	1199
DB	1273	ATCAAAATCCAGATGTGCTCTTATTTCCCATGAAAAAGTCTCATGATATTTGAGAA	1332
QY	1200	GACCTACTTACAAAGTGGCATATA-TTGCAATTTATTTTAAATAAAGATCACTATTAT	1258
DB	1333	GACCTACTTACAAAGTGGCATATA-TTGCAATTTATTTTAAATAAAGATCACTATTAT	1392
QY	1259	ATATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTGAGG	1318
DB	1393	ATATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTGAGG	1452
QY	1319	GTGGCAGTATAGTGAATTTCTTTTAAATTTCTGTTAAATTTATCTGATTTTCTAAAT	1378
DB	1453	GTGGCAGTATAGTGAATTTCTTTTAAATTTCTGTTAAATTTATCTGATTTTCTAAAT	1512
QY	1379	CTAATGAAGATGAATTCCTTGTATATAAATAAAGAAAGAAATTAATCTTGAGTAAGC	1438
DB	1513	CTAATGAAGATGAATTCCTTGTATATAAATAAAGAAAGAAATTAATCTTGAGTAAGC	1572
QY	1439	AGAGCAGACATCATCTCTGATTTGCTCAGCCTCAATTTCCCGAGTAAATTTCAATTTG	1498
DB	1573	AGAGCAGACATCATCTCTGATTTGCTCAGCCTCAATTTCCCGAGTAAATTTCAATTTG	1632
QY	1499	AATCGAGCTCTGCTCTCTGTTGTTGTTAGTAGTGTGATCAGGAAACAGATCTCAGCAAAG	1558
DB	1633	AATCGAGCTCTGCTCTCTGTTGTTGTTAGTAGTGTGATCAGGAAACAGATCTCAGCAAAG	1692
QY	1559	CACTGAGGAGAGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA	1618
DB	1693	CACTGAGGAGAGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA	1752
QY	1619	AGACAAAATCATCTGCTTAATTTCTTCTAGAGGATCACAGCCCTGGGATTTCAAGG	1678
DB	1753	AGACAAAATCATCTGCTTAATTTCTTCTAGAGGATCACAGCCCTGGGATTTCAAGG	1812
QY	1679	CATTGGATTCAGTCTCTAAGAGGCTGTGCTACTGTTGAAATTTGTCTCCCTCAAAATTC	1738
DB	1813	CATTGGATTCAGTCTCTAAGAGGCTGTGCTACTGTTGAAATTTGTCTCCCTCAAAATTC	1872
QY	1739	ACATCCTTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATGAAGGTCTCTGCAGATGA	1798

[illegible]

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RESULT 9
US-09-41
; Sequence
; Patent
; GENERAL
; APPLIC
; APPLIC
; TITLE
; FILE N
; CURREN

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APPLICANT: PAGE, ANH
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36328
CURRENT APPLICATION NUMBER: US/09/417.455

6723	GAAGGATCACAGCCCCTGGGATTTCCAAAGGCAATGGATCCAGTCTCTTAAGAAAGGCTGCTGT	6787
1710	ACTGGTTGAATTTGTGTCCTCCCTCAAAATTACATCCCTTTCTTGGAAATCTCAGTCTGTGAGTT	1769
6783	ACTGGTTGAATTTGTGTCCTCCCTCAAAATTACATCCCTTTCTTGGAAATCTCAGTCTGTGAGTT	6842
1770	TATTTGAGATAAGGCTCTCTGCAGATGTAGTTAGTTAAAGACAAGGTCATGCTGGATGAAG	1829
6843	TATTTGAGATAAGGCTCTCTGCAGATGTAGTTAGTTAAAGACAAGGTCATGCTGGATGAAG	6902
1830	GTAGACCTAAATTCATATGACTGTGGTTTCCTGTATGATAAAGAGAGAGACACAGAGACAG	1889
6903	GTAGACCTAAATTCATATGACTGTGGTTTCCTGTATGATAAAGAGAGAGACACAGAGACAG	6962
1890	AGGAGACGGGGGAAGACTATGTAAAGATGAAGGACAGAGATCGGAGTTTTCAGCCACAA	1949
6963	AGGAGACGGGGGAAGACTATGTAAAGATGAAGGACAGAGATCGGAGTTTTCAGCCACAA	7022
1950	GCTAAGAAACACCAAGGATTTGGCCAAACCATCAGAAAGCTTTGGAAGAGCGCAAGAAAT	2009
7023	GCTAAGAAACACCAAGGATTTGGCCAAACCATCAGAAAGCTTTGGAAGAGCGCAAGAAAT	7082
2010	CTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAG	2069
7083	CTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAG	7142
2070	CCTCCTGAAAGAAAGAAATAATTTCCGCTGTGTTTAAAGCCACCAAGAGATAATTCGTTA	2129
7143	CCTCCTGAAAGAAAGAAATAATTTCCGCTGTGTTTAAAGCCACCAAGAGATAATTCGTTA	7202
2130	CAGCAGCTCTAGGAAACTAATACAGCTGCTTAAATGATCCCTGTCTCTCGTGTTTACAT	2189
7203	CAGCAGCTCTAGGAAACTAATACAGCTGCTTAAATGATCCCTGTCTCTCGTGTTTACAT	7262
2190	TCTGTGTGTGCCCTCCCAACAATGTACCAAGTTGTCTTTGTGACCCCAATAGAAATATGG	2249
7263	TCTGTGTGTGCCCTCCCAACAATGTACCAAGTTGTCTTTGTGACCCCAATAGAAATATGG	7321
2250	CAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAGACACTGCAGCTTCTACATT	2309
7322	CAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAGACACTGCAGCTTCTACATT	7381
2310	GAGCCCTCTCTCTGTGCCACCAACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGG	2369
7382	GAGCCCTCTCTCTGTGCCACCAACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGG	7441
2370	AAGCTAGCTGCCATGCTATGAGGAGCCCTATAAAGAGACTTACGTTGTTAAAAATGAAGT	2429
7442	AAGCTAGCTGCCATGCTATGAGGAGCCCTATAAAGAGACTTACGTTGTTAAAAATGAAGT	7501
2430	CTCCTCCACAGCCACATTTAGTGAACCTTAGAAGCAGAGACTCTGTGAGATAATCGATCT	2489
7502	CTCCTCCACAGCCACATTTAGTGAACCTTAGAAGCAGAGACTCTGTGAGATAATCGATCT	7561
2490	TTGTTGTTTTAAAGTTGCTCAGTTTTTGGTCTAACTTGTATGCGCAATAGATAAATA	2549
7562	TTGTTGTTTTAAAGTTGCTCAGTTTTTGGTCTAACTTGTATGCGCAATAGATAAATA	7621
2550	TGCAGAGAAAGAGA	2563
7622	TGCAGAGAAAGAGA	7635

Query Match	86.6%	Score 2220.4	DB 3	Length 7605
Best Local Similarity	99.1%	Pred. No. 0		
Matches 2274	Conservative 0	Mismatches 16	Indels 4	Gaps 4
Qy	271	AGCCAGTGAACATCATGAGAGCTCTATCTTGGTGCACAGGAATCCAAAGAGCTTCACCTTCT	330	
Db	5105	AGCCAGTGAACATCATGAGAGCTCTAATCTTGGTGCCAGGAATCCAAAGAGCTTCACCTTCT	5164	
Qy	331	ACCGGGGGGACATGGGGGCTCACCTCCAGCTTCGAGTCGGCTGCTACCCGGGCTGGTTCC	390	
Db	5165	ACCGGGGGGACATGGGGGCTCACCTCCAGCTTCGAGTCGGCTGCTACCCGGGCTGGTTCC	5224	
Qy	391	TGTGCAAGGTGCTGAAGCCGATCAGCCTCTCAGACTCACCCAGCTTCCCGGAGAAATGGTG	450	
Db	5225	TGTGCAAGGTGCTGAAGCCGATCAGCCTCTCAGACTCACCCAGCTTCCCGGAGAAATGGTG	5284	
Qy	451	GCTGGAAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAACGTGCCCC	510	
Db	5285	GCTGGAAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAACGTG-CCC	5343	
Qy	511	CCCGAATCTCCCTGGGAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG	570	
Db	5344	CCCGAATCTCCCTGGGAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG	5403	
Qy	571	GACAATCACTCTTTCTGCTCTCAGGACCCCCAGGCTCTGACTTAAGTGGGCACTTGACCACT	630	
Db	5404	GACAATCACTCTCTCTGCTCTCAGGACCCCCAGGCTCTGACTTAAGTGGGCACTTGACCACT	5463	
Qy	631	TTGTCTTCGGTCCCAAGTTTGCATAAATCTCAGATTTGGAGCTCAGTCCAGGGTCTCTC	690	
Db	5464	TTGTCTTCGGTCCCAAGTTTGGATAAATCTCAGATTTGGAGCTCAGTCCAGGGTCTCTC	5523	
Qy	691	CCCCACTGGATGGTGCTACTGCTGTGAACTTTGTAAACCACCATGTGGGGTAACTGGGA	750	
Db	5524	CCCCACTGGATGGTGCTACTGCTGTGAACTTTGTAAACCACCATGTGGGGTAACTGGGA	5583	
Qy	751	ATAACATGAAAAAGATTTCTGTGGGGGTGGGGGTGGGGAGTGTCTGGGGAATCATTTCTGCTT	810	
Db	5584	ATAACATGAAAAAGATTTCTGTGGGGGTGGGGGTGGGGAGTGTCTGGGGAATCATTTCTGCTT	5643	
Qy	811	AATGGTAACTGACAGTGTTTACCTCAGACCCCGCAGGCCAACCCATCCCAAGTTGACCT	870	
Db	5644	AATGGTAACTGACAGTGTTTACCTCAGACCCCGCAGGCCAACCCATCCCAAGTTGACCT	5703	

Db 6783 GCTAAGAAACACCAAGGATTTGTGGCAACCATCAGAAAGCTTGAAGAGGCAAGAAAT 6842
QY 2010 CTTCCCTAGAGGCTTTAGAGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAG 2069
Db 6843 CTTCCCTAGAGGCTTTAGAGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAG 6902
QY 2070 CTTCCCTAGAGGATAAATTTCCGCTGCTTTTAAAGCCACCAAGGATAATTTGGTTA 2129
Db 6903 CTTCCCTAGAGGATAAATTTCCGCTGCTTTTAAAGCCACCAAGGATAATTTGGTTA 6962
QY 2130 CAGCAGCTCTAGAAACTTAATCAGCTGCTGAAATGATCCCTGCTCTCTGCTGTTTACAT 2189
Db 6963 TGGCAGCTCTAGGAAACTTAATCAGCTGCTGAAATGATCCCTGCTCTCTGCTGTTTACAT 7022
QY 2190 TCTGCTGTGTCCCTCCACCAATGACCAAGTGTCTTTTGGAGCCCAATAGATATGG 2249
Db 7023 TCTGCTGTGTCCCTCCACCAATGACCAAGTGTCTTTTGGAGCCCAATAGATATGG 7081
QY 2250 CAGAAGTGTATGCGATGCCACTTCCAAAGATTAGGTTATATAAGACACTGCAGCTTCTACTT 2309
Db 7082 CAGAAGTGTATGCGATGCCACTTCCAAAGATTAGGTTATATAAGACACTGCAGCTTCTACTT 7141
QY 2310 GAGCCCTCTCTCTGCGCAACCCACCCGCTTATCTTCTGCTCACTGCTCTGCGGG 2369
Db 7142 GAGCCCTCTCTCTGCGCAACCCACCCGCTTATCTTCTGCTCACTGCTCTGCGGG 7201
QY 2370 AAGCTAGCTGCCATGCTATGAGCAGGCTTATAGAGACTTACGTTGTAATAAATCAAGT 2429
Db 7202 AAGCTAGCTGCCATGCTATGAGCAGGCTTATAGAGACTTACGTTGTAATAAATCAAGT 7261
QY 2430 CTCCTGCCACAGCCACTTAGTGAACCTAGAGCAGAGACTCTGTGAGATAATCGATCT 2489
Db 7262 CTCCTGCCACAGCCACTTAGTGAACCTAGAGCAGAGACTCTGTGAGATAATCGATCT 7321
QY 2490 TTGTTCTTTAAGTTGCTCAGTTTGGCTTAATCTTGTATGAGCAGAAATAGATAAATA 2549
Db 7322 TTGTTCTTTAAGTTGCTCAGTTTGGCTTAATCTTGTATGAGCAGAAATAGATAAATA 7381
QY 2550 TGCAGAGAAAGAGA 2563
Db 7382 TGCAGAGAAAGAGA 7395

RESULT 10
US-09-348-942-8
; Sequence 8, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-348-942-8

Query Match 86.6%; Score 2220.4; DB 3; Length 7605;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2274; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

QY 271 ACCAGTGAACATCATGAGCTCTATCTTGTGGCCAAAGAAATCCAAGAGCTTCACTTCT 330
Db 5105 AGCCAGTGAACATCATGAGCTCTATCTTGTGGCCAAAGAAATCCAAGAGCTTCACTTCT 5164
QY 331 ACCGGCGGACATGAGGCTCACCTCCAGCTTCGAGTCGCTCCCTACCGGGCTGTTCC 390
Db 5165 ACCGGCGGACATGAGGCTCACCTCCAGCTTCGAGTCGCTCCCTACCGGGCTGTTCC 5224
QY 391 TGTGACACGCTGCTGAAAGCCGATCAGCTCTCAGACTCACCCAGCTTCCCGAGAATGGTG 450
Db 5225 TGTGACACGCTGCTGAAAGCCGATCAGCTCTCAGACTCACCCAGCTTCCCGAGAATGGTG 5284
QY 451 GGTGAATGCCCCCATCAAGACTTCTACTTCCAGAGTGTGACTAGGGCAACGTGCCCC 510
Db 5285 GGTGAATGCCCCCATCAAGACTTCTACTTCCAGAGTGTGACTAGGGCAACGTGCCCC 5343
QY 511 CCCAGAACTCCCTGGGAGAGCCAGCTCGGTGAGGGGTGAGTGAGGAGAGCCCATGGCG 570
Db 5344 CCCAGAACTCCCTGGGAGAGCCAGCTCGGTGAGGGGTGAGTGAGGAGAGCCCATGGCG 5403
QY 571 GACAACTCACTCTTCTGCTCTCAGAGCCGCCAGGTCTGACTTTAGTGGGCACCTGACCACT 630
Db 5404 GACAACTCACTCTCTGCTCTCAGAGCCGCCAGGTCTGACTTTAGTGGGCACCTGACCACT 5463
QY 631 TTGCTTCTGCTTCCAGTTTGTGATAAATCTGAGATTGAGAGCTCAGTCCAGGCTCTC 690
Db 5464 TTGCTTCTGCTTCCAGTTTGTGATAAATCTGAGATTGAGAGCTCAGTCCAGGCTCTC 5523
QY 691 CCCCACTGGATGGTGTACTGCTGTGGAACCTTGTAAACCAATCTGGGGTAAACCTGGGA 750
Db 5524 CCCCACTGGATGGTGTACTGCTGTGGAACCTTGTGTAAACCAATCTGGGGTAAACCTGGGA 5583
QY 751 ATAAACATGAAAGATTTCTGTGGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGCTT 810
Db 5584 ATAAACATGAAAGATTTCTGTGGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGCTT 5643
QY 811 AATGTAACTGACAAAGTGTATACCTGAGCCCGCAGGCAACCCATCCCCAGTTGAGCT 870
Db 5644 AATGTAACTGACAAAGTGTATACCTGAGCCCGCAGGCAACCCATCCCCAGTTGAGCT 5703
QY 871 TATAGGTCAGTGTAGCTCTCCACATGAAGTCTCTCAGCTCAGAGATAAAGATAAGTAGGGTAT 930
Db 5704 TATAGGTCAGTGTAGCTCTCCACATGAAGTCTCTCAGCTCAGAGATAAAGATAAGTAGGGTAT 5763
QY 931 GTGGTCATAGAGTCAAGGATCTATGGCCCTTGGCCAGCCGCCACCCCTTCCCTTT-ATC 989
Db 5764 GTGGTCATAGAGTCAAGGATCTATGGCCCTTGGCCAGCCGCCACCCCTTCCCTTTAATC 5823
QY 989 GTGCCACTGTCAATGCTACCTTCTCTATCTCTTCCCTCATCATCTTGTGTGGGATGA 1049
Db 5824 GTGCCACTGTCAATGCTACCTTCTCTATCTCTTCCCTCATCATCTTGTGTGGGATGA 5883
QY 1050 GGAGGTGTGTGTCAGAAAGAAATGGTTCGAGCTCAGAGATAAAGATAAGTAGGGTAT 1109
Db 5884 GGAGGTGTGTGTCAGAAAGAAATGGTTCGAGCTCAGAGATAAAGATAAGTAGGGTAT 5943
QY 1110 GCTGATCTCTTTTAAAAAACCAGATACAAATCAAAATCCAGATGCTGCTCTATTCC 1169
Db 5944 GCTGATCTCTTTTAAAAAACCAGATACAAATCAAAATCCAGATGCTGCTCTATTCC 6003
QY 1170 CATGAAAAAGTGTCTCATATATTGAGAGACCTTCTTACAAAGTGGCATATATTGAA 1229

5165	ACC	GCGGGG	CATGGGG	CTCACCTT	CCAGCTTC	CGAGTC	GGCTGAC	CCACCGGGG	CTGCTTCC	5224
391	TGT	GCA	CGGTG	CTGAA	CCGATCAG	CCCTGT	CAGACT	CACCCAGCTT	CCCCAGAAATGGT	450
5225	TGT	GAC	CGGTG	CCTGA	AGCCGATCAG	CCCTGT	CAGACT	CACCCAGCTT	CCCCAGAAATGGT	5284
451	GCT	GAAATGCC	CCCATCAC	GACTTCTA	CTTCCAGCAGTGT	GA	CTAGGG	GCNA	CGTGC	510
5285	GCT	GAAATGCC	CCCATCAC	GACTTCTA	CTTCCAGCAGTGT	GA	CTAGGG	GCNA	CGTGC	5343
511	CCC	GAAATC	CTCCTGG	CAGAC	CCAGCTCG	GGTGAGGG	TGAGT	CGAGAGAC	CCCATGGCG	570
5344	CCC	GAAATC	CTCCTGG	CAGAC	CCAGCTCG	GGTGAGGG	TGAGT	CGAGAGAC	CCCATGGCG	5403
571	GAC	AATCA	CTCTTCT	CTGCTC	TAGGAC	CCCCCAG	CTCTGA	CTTAGT	GGCACCTG	630
5404	GAC	AATCA	CTCTCT	CTGCTC	TAGGAC	CCCCCAG	CTCTGA	CTTAGT	GGCACCTG	5463
631	TTG	CTCTCG	TTCC	CAGTTT	GTGCATAA	TTCTGAGAT	TTTGGAG	CTCAGT	CCAGGTCCTC	690
5464	TTG	CTCTCG	TTCC	CAGTTT	GTGCATAA	TTCTGAGAT	TTTGGAG	CTCAGT	CCAGGTCCTC	5523
691	CCC	CACTGG	ATG	TGCTCT	GTGAA	CCCTTGT	TAAAA	CCATGT	GGGTAA	750
5524	CCC	CACTGG	ATG	TGCTCT	GTGAA	CCCTTGT	TAAAA	CCATGT	GGGTAA	5583
751	ATA	CACTGAA	AAAGAT	TTCTG	TGGGGTGG	GGTGGG	GAGT	CTGG	GNATCA	810
5584	ATA	CACTGAA	AAAGAT	TTCTG	TGGGGTGG	GGTGGG	GAGT	CTGG	GNATCA	810
811	AAT	GGTA	CTGAC	AAAGTT	TACCTG	AGCCCCG	CAGCC	CAAC	CTCC	870
5644	AAT	GGTA	CTGAC	AAAGTT	TACCTG	AGCCCCG	CAGCC	CAAC	CTCC	870
871	TAT	AGGCTC	AGTAG	CTCC	CACATGA	AGTCTCT	CACT	CACCA	CTGT	930
5704	TAT	AGGCTC	AGTAG	CTCC	CACATGA	AGTCTCT	CACT	CACCA	CTGT	5763
931	GTG	GTCA	TAGAGT	CAGG	GATCTAT	GGCCCTT	GGCCAG	CCCCC	CTTCC	989
5764	GTG	GTCA	TAGAGT	CAGG	GATCTAT	GGCCCTT	GGCCAG	CCCCC	CTTCC	5823
990	CTG	CCACTG	CTAT	GTCT	CTCTTCC	TATCTCT	TTCCCT	CA	TAATCT	1049
5824	CTG	CCACTG	CTAT	GTCT	CTCTTCC	TATCTCT	TTCCCT	CA	TAATCT	5883
1050	GG	AGTG	GTGAT	GT	CAGAA	AAATGG	TTCCAG	CTC	AGAGATA	1109
5884	GG	AGTG	GTGAT	GT	CAGAA	AAATGG	TTCCAG	CTC	AGAGATA	5943
1110	GCT	GATC	CTCTTT	TAAAA	CCCAAG	TACAAT	CAAAAT	CCC	CAGAT	1169
5944	GCT	GATC	CTCTTT	TAAAA	CCCAAG	TACAAT	CAAAAT	CCC	CAGAT	6003
1170	CAT	GAAAA	AGTG	CTAT	GTAG	AGAC	CTTAC	AAAGT	GGCATAT	1229
6004	CAT	GAAAA	AGTG	CTAT	GTAG	AGAC	CTTAC	AAAGT	GGCATAT	6063
1230	TTT	ATTTAA	TAAAA	GATAC	CTTATTT	TATATATTT	CTTTAT	TAGAAAA	AAAGT	1289
6064	TTT	ATTTAA	TAAAA	GATAC	CTTATTT	TATATATTT	CTTTAT	TAGAAAA	AAAGT	6123
1290	TTTT	ACTCA	ATTTAG	CAAT	TGTCAG	GGTGG	CAGTATAG	GTGAT	TTTTTT	1349
6124	TTTT	ACTCA	ATTTAG	CAAT	TGTCAG	GGTGG	CAGTATAG	GTGAT	TTTTTT	6183
1350	TGT	TAATTT	TATCTG	TATTTCT	CTAA	TTTCTCA	AAATGA	AGATGA	ATTTCT	1409
6184	TGT	TAATTT	TATCTG	TATTTCT	CTAA	TTTCTCA	AAATGA	AGATGA	ATTTCT	6243
1410	TAA	GAAAGAA	ATTA	CTTG	AGTAA	GACG	AGAC	ATCA	CTCT	1469
6244	TAA	GAAAGAA	ATTA	CTTG	AGTAA	GACG	AGAC	ATCA	CTCT	6302

QY	1470	CTCCAAATTTCCCGACAGATAAATTCAAATTGAATCGAGCTCTGCTGCTCTGTTGGTTGTAG	1522
DB	6303	CTCCACTTTCCCGACAGATAAATTCAAATTGAATCGAGCTCTGCTGCTCTGTTGGTTGTAG	6362
QY	1530	TAGTGATCAGAAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGTG	1589
DB	6363	TAGTGATCAGAAATCAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGATGAGTTTGTG	6422
QY	1590	TGGCTTGGAAATCTCTGGGTAAAGAACTTTAAAGAAACAAATAATCATCTGGTAATCTTTCCCTA	1649
DB	6423	TGGCTTGGAAATCTCTGGGTAAAGAACTTTAAAGAAACAAATAATCATCTGGTAATCTTTCCCTA	6482
QY	1650	GAAGGATCAGACCCCTCTGGGATTTCAAAGGCAATTTGGATTCAGTCTCTAAGAAAGCTGCTGT	1709
DB	6483	GAAGGATCAGACCCCTCTGGGATTTCAAAGGCAATTTGGATTCAGTCTCTAAGAAAGCTGCTGT	6542
QY	1710	ACTGGTTGAAATTTGTCTCCCTCAAAATTCACATCCCTTTTGGAAATCTCAGTCTGTGAGTT	1769
DB	6543	ACTGGTTGAAATTTGTCTCCCTCAAAATTCACATCCCTTTTGGAAATCTCAGTCTGTGAGTT	6602
QY	1770	TATTTGGAGATAAGGTCTCTGCGAGATGTAGTTAGTTAAAGACAAGGTCAATGCTGGATGAAG	1829
DB	6603	TATTTGGAGATAAGGTCTCTGCGAGATGTAGTTAGTTAAAGACAAGGTCAATGCTGGATGAAG	6662
QY	1830	GTAGACCTTAATTCAAATATCAGCTGGTTTCTCTGTATGAAAGAGGAGGACACAGAGACAG	1889
DB	6663	GTAGACCTTAATTCAAATATCAGCTGGTTTCTCTGTATGAAAGAGGAGGACACAGAGACAG	6722
QY	1890	AGGAGACGCGGGGAAGACTATGTAAAGATGAAGGCAGAGATCGGAGTTTTTGCAGCCACAA	1949
DB	6723	AGGAGACGCGGGGAAGACTATGTAAAGATGAAGGCAGAGATCGGAGTTTTTGCAGCCACAA	6782
QY	1950	GCTAAGAAACACCAAGATTTGTGCGCAACCATCAGAAGCTTTGAAAGAGCAAGAAGAAAT	2009
DB	6783	GCTAAGAAACACCAAGATTTGTGCGCAACCATCAGAAGCTTTGAAAGAGCAAGAAGAAAT	6842
QY	2010	CTTCCCTTAGAGGCTTTAGAGGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAG	2069
DB	6843	CTTCCCTTAGAGGCTTTAGAGGGATAACGGCTCTGCTGACACCTTAATCTCAGACTTCCAG	6902
QY	2070	CCTCCTGAAAGAAAGAAATAATTTTCGGCTGTTTTAAGCCACAAGATAATTTGGTTA	2129
DB	6903	CCTCCTGAAAGAAAGAAATAATTTTCGGCTGTTTTAAGCCACCAGAGATAATTTGGTTA	6962
QY	2130	CAGCAGCTCTAGAAACTAATACAGCTGCTAAAATGATCCCTGCTCTCTCGTGTTTACAT	2189
DB	6963	TGGCAGCTCTAGAAACTAATACAGCTGCTAAAATGATCCCTGCTCTCTCGTGTTTACAT	7022
QY	2190	TCTGTGTGTCTCCCTCCCACAATGTACCAAAAGTTGTCTTTGTGACCCCAATAGAAATGG	2249
DB	7023	TCTGTGTGTCTCCCTCCCACAATGTACCAAAAGTTGTCTTTGTGA - CCAATAGAAATAGG	7081
QY	2250	CAGAAAGTATGGCATGCCACTTCCAAGATTTAGGTTATAAAGACACTCGAGCTTCTACTT	2309
DB	7082	CAGAAAGTATGGCATGCCACTTCCAAGATTTAGGTTATAAAGACACTCGAGCTTCTACTT	7141
QY	2310	GAGCCCTCTCTCTGCGCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG	2369
DB	7142	GAGCCCTCTCTCTGCGCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG	7201
QY	2370	AAGCTAGCTGCCATGTATGAGCAGGCTTATAAAGAGACTTACGPGGTAAAAATGAAGT	2439
DB	7202	AAGCTAGCTTCCAATGTATGAGCAGGCTTATAAAGAGACTTATGTGTGTAAAAATGAAGT	7261
QY	2430	CTCTGCGCCACGCCACATTTAGTGAACCTTAGAAGCAGAGACTCTGTGAGATAATCGATGT	2489
DB	7262	CTCTGCGCCACGCCACATTTAGTGAACCTTAGAAGCAGAGACTCTGTGAGATAATCGATGT	7321
QY	2490	TTGTGTGTTTAAAGTCTCAGTTTTTGGTCTAACTTTGTATTATCAGCAATAGATAATAATA	2549
DB	7322	TTGTGTGTTTAAAGTCTCAGTTTTTGGTCTAACTTTGTATTATCAGCAATAGATAATAATA	7381

5344	CCCNAGAACTCCCTGGGCAGAGCCACGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG	5403	
Qy	751	GACAATCACTCTTTTCTGCTCTCAGGACCCCCAGGCTGTGACTTGTAGTGGCACCTGACCACT	630
Db	5404	GACAATCACTCTCTCTGCTCTCAGGACCCCCACGCTCTGACTTGTAGTGGCACCTGACCACT	5463
Qy	631	TTGTCTTCTGGTTCGCCAGTTTGCATAAATTTCTGAGATTTTGGAGCTCAGTCCAGGGTCCCTC	690
Db	5464	TTGTCTTCTGGTTCGCCAGTTTGGATAAATTTCTGAGATTTTGGAGCTCAGTCCACGGTCCCTC	5523
Qy	691	CCCACATGGATGGTGTCTACTGCTGTGGAACTCTGTAAAAACCATGTGGGGTAAACTGGGA	750
Db	5524	CCCACATGGATGGTGTCTACTGCTGTGGAACTCTGTGTAAAAACCATGTGGGGTAAACTGGGA	5583
Qy	751	ATAACATGAAAAAGATTTTCTGTGGGGGTGGGTGGGGAGTGTCTGGGAATCATTTCTCTGTT	810
Db	5584	ATAACATGAAAAAGATTTTCTGTGGGGGTGGGTGGGGAGTGGTGGGAATCATTTCTCTGTT	5643
Qy	811	AATGGTAACTGACAAAGTTTACCTGTAGCCCGCAGCGAGCCAAACCATCCCCCAGTTGAGCCT	870
Db	5644	AATGGTAACTGACAAAGTTTACCTGTAGCCCGCAGCGAGCCAAACCATCCCCCAGTTGAGCCT	5703
Qy	871	TATAGGGTCAGTAGTCTCTCCACATGAAGTCTCTCTCACTCAACACTGTGACGAGAGGGAG	930
Db	5704	TATAGGGTCAGTAGTCTCTCCACATGAAGTCTCTCTCACTCAACACTGTGACGAGAGGGAG	5763
Qy	931	GTGTCATAGAGTCAGGGATCTATGGGCCCTTGGCCACGCCCCACCCCTTCCCTTT-ATC	989
Db	5764	GTGTCATAGATCAGGGATCTATGGGCCCTTATGGCCACGCCCCACCCCTTCCCTTTAATC	5823
Qy	990	CTGCCACTGTCATATGCTACTCTTCTCTCATCTCTTCCCTCATCATCTTGTGTGGGCATGA	1049
Db	5824	CTGCCACTGTCATATGCTACTCTTCTCTCATCTCTTCCCTCATCATCTTGTGTGGGCATGA	5883
Qy	1050	GGAGTGGTCATGTGCAGAAAGATGGTTCAGAGCTCAGAAGATAAAGATAAGTAGGGTAT	1109
Db	5884	GGAGTGGTGTATGTGCAGAAAGATGGTTCAGAGCTCAGAAGATAAAGATAAGTAGGGTAT	5943
Qy	1110	GCTGATCCTCTTTTAAAAACCCAGATACAAATCAAAATCCACAGTCTGCTCTATTTC	1169
Db	5944	GCTGATCCTCTTTTAAAAACCCAGATACAAATCAAAATCCACAGTCTGCTCTATTTC	6003
Qy	1170	CATGAAAAAGTGTCTATGACATATTGAGAGAGCCTACTTACAAAGTGGCATATATTGCAA	1229
Db	6004	CATGAAAAAGTGTCTATGACATATTGAGAGAGCCTACTTACAAAGTGGCATATATTGCAA	6063
Qy	1230	TTTTATTTTAAATAAGATACCTATTTATATATTTCTTTTATAGAAAAAGTCTGGAAG	1289
Db	6064	TTTTATTTTAAATAAGATACCTATTTATATATTTCTTTTATAGAAAAAGTCTGGAAG	6123
Qy	1290	TTTACTTCAATTTGAGCAATGTCCAGGTGGTGGCAGTATAGGTGATTTTTCTTTTAAATTC	1349
Db	6124	TTTACTTCAATTTGAGCAATGTCCAGGTGGTGGCAGTATAGGTGATTTTTCTTTTAAATTC	6183
Qy	1350	TGTTAAATTTATCTATTTTCTTAATTTTCTACAATGAAGATGAATTTCTTGTTATAAAAA	1409
Db	6184	TGTTAAATTTATCTATTTTCTTAATTTTCTACAATGAAGATGAATTTCTTGTTATAAAAA	6243
Qy	1410	TAGAAAAAGAAATTAATCTTTGAGGTATAGCAGAGCAGACATCACTCTGATTTGCTCTCAGC	1469
Db	6244	TAGAAAAAGAAATTTAATCTTTGAGGTATAGCAGAGCAGACATCACTCTGATTTG-CTCAGC	6302
Qy	1470	CTCCAAATTTCCCGAGAGTAAATTCAAATTTGAATCGAGCTCTGCTGCTCTGGTGGTGTAG	1529
Db	6303	CTCCAAATTTCCCGAGAGTAAATTTCAATTTGAATCGAGCTCTGCTGCTCTGGTGGTGTAG	6362
Qy	1530	TAGTGATCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGTG	1589
Db	6363	TAGTGATCAGGAAATCAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGATGAGTTTGTG	6422
Qy	1590	TGGCTGGAATCTCTGGGTAAAGAACTTAAAGAACAAAAATCATCTGGTAAATCTTTTCCTA	1649
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Db 4552 ATAAATGAAAGATTCTGTGGGGTGGGGTGGGGAGTGGTGGGAATCATCTCTGCTT 4611
QY 811 AATGGTAACTGACAACTGTTTACCTCTGAGCCGCCAGCCCAACCATCCCAAGTTAGCCT 870
Db 4612 AATGGTAACTGACAACTGTTTACCTCTGAGCCGCCAGCCCAACCATCCCAAGTTAGCCT 4671
QY 871 TATAGGGTCAGTAGCTCTCCACATGAAGTCTCTCACTACCACTGTGAGGAGGGAG 930
Db 4672 TATAGGGTCAGTAGCTCTCCACATGAAGTCTCTCACTACCACTGTGAGGAGGGAG 4731
QY 931 GTGGTCATAGAGTCAGGAGTCTATGCGCTTGGCTTGGCCAGCCCAACCCCTTCCCTTT-ATC 989
Db 4732 GTGGTCATAGAGTCAGGAGTCTATGCGCTTGGCCAGCCCAACCCCTTCCCTTTAATC 4791
QY 990 CTGCCACTGTCAATGCTACCTTCTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGA 1049
Db 4792 CTGCCACTGTCAATGCTACCTTCTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGA 4851
QY 1050 GGAGGTGGTGAATGTCAGAAAGAAATGGTTCGAGCTCAGAAAGATAAAAGATAAGTAGGGTAT 1109
Db 4852 GGAGGTGGTGAATGTCAGAAAGAAATGGTTCGAGCTCAGAAAGATAAAAGATAAGTAGGGTAT 4911
QY 1110 GCTGATCTCTTTTAAAAACCCAGATACAAAT-CCAGATGCTGCTCTATTTC 1168
Db 4912 GCTGATCTCTTTTAAAAACCCAGATACAAATCAAAATCCCAAGATGCTGCTCTATTTC 4971
QY 1169 CCATGAAAAAGTCTCATGACATATTGAGAGACCTTACTACAAAGTGCATATATTGCA 1228
Db 4972 CCATGAAAAAGTCTCATGACATATTGAGAGACCTTACTACAAAGTGCATATATTGCA 5031
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Db 5032 ATTTATTTTAAATTAAGATACCTATTTATATATTTCTTTATAGAAAAAGTCTGGAAGA 5091
QY 1289 GTTTACTTCAATGTAGCAATGTGAGGTGGTGGCAGATAGGTGATTTTCTTTTAAAT 1348
Db 5092 GTTTACTTCAATGTAGCAATGTGAGGTGGTGGCAGATAGGTGATTTTCTTTTAAAT 5151
QY 1349 CTGTTAAATTTCTGTATTTCTTAAATTTTCTACAAATGAAGTGAATTCCTGTATATAA 1408
Db 5152 CTGTTAAATTTCTGTATTTCTTAAATTTTCTACAAATGAAGTGAATTCCTGTATATAA 5211
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Db 5212 ATAGAAAAAGAAATTAATCTGAGGTAAAGCAGAGCAGACATCATCTCTGATKG-CTCTAG 5270
QY 1469 CTCTCAATTTCCCAAGTAAATTCAAATTCAAATTCGAGCTCTGCTCTCTGGTTGGTTGA 1528
Db 5271 CTCTCAATTTCCCAAGTAAATTCAAATTCGAGCTCTGCTCTCTGGTTGGTTGA 5330
QY 1529 GTAGTGATCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGCGTGTGAGTTTCT 1588
Db 5331 GTAGTGATCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGCGTGTGAGTTTCT 5390
QY 1589 GTGGCTGGAATCTCTGGGTAAAGAACTTAAAGAAACAAATCATCTGTAATTTCTTCT 1648
Db 5391 GTGGCTGGAATCTCTGGGTAAAGAACTTAAAGAAACAAATCATCTGTAATTTCTTCT 5450
QY 1649 AGAAGGATCAGACGCCCTCGGATTTCAAGGCATTTGGATCCAGTCTCTAAGAAAGCTGCTG 1708
Db 5451 AGAAGGATCAGACGCCCTCGGATTTCAAGGCATTTGGATCCAGTCTCTAAGAAAGCTGCTG 5510
QY 1709 TACTGTTGAAATGTTGTCCTTCAAAATTCACATCTCTTGGAAATCTCAGTCTGTGAGT 1768
Db 5511 TACTGTTGAAATGTTGTCCTTCAAAATTCACATCTCTTGGAAATCTCAGTCTGTGAGT 5570
QY 1769 TTATTTGGAGATAGGCTCTCTGAGATGTAGTTAGTTTAAACAAGCTCATGCTGGATGAA 1828
Db 5571 TTATTTGGAGATAGGCTCTCTGAGATGTAGTTTAAACAAGCTCATGCTGGATGAA 5630
QY 1829 GGTAGACCTTAAATTTCAATATGACTGTTTCTTGTATGAAAGGAGGACACAGAGACA 1888

Db 5631 GGTAGACCTTAAATTTAATATGACTGTTTCTTGTATGAAAGGAGGACACAGAGACA 5690
QY 1889 GAGGAGACCGGGGAGAGACTATGTAAGATGAAGGAGAGATCGGAGTTTTCAGGCCACA 1948
Db 5691 GAGGAGACCGGGGAGAGACTATGTAAGATGAAGGAGAGATCGGAGTTTTCAGGCCACA 5750
QY 1949 A 1949
Db 5751 A 5751
RESULT 14
US-09-348-942-7
; Sequence 7, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 5751
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(5751)
; OTHER INFORMATION: n = A,T,C or G
US-09-348-942-7

Query Match 63.1%; Score 1616.6; DB 3; Length 5751;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1663; Conservative 5; Mismatches 9; Indels 4; Gaps 4;
QY 271 AGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAGGAATCCAGAGCTTCACCTTCT 330
Db 4073 AGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAGGAATCCAGAGCTTCACCTTCT 4132
QY 331 ACCGGCGGACATGGGGCTCACCTCCAGTTCGAGTCGGCTCGCTACCCGGGCTGGTTCC 390
Db 4133 ACCGGCGGACATGGGGCTCACCTCCAGTTCGAGTCGGCTCGCTACCCGGGCTGGTTCC 4192
QY 391 TGTGACGGTGCCTGAAGCCGATCAGCTCAGACTCACCAGCTTCCGAGAAATGGTG 450
Db 4193 TGTGACGGTGCCTGAAGCCGATCAGCTCAGACTCACCAGCTTCCGAGAAATGGTG 4252
QY 451 GCTGGAATGCCCCCATCACAGACTTCTACTCCAGCAGTGTGACTAGGCAACGTCSCCCC 510
Db 4253 GCTGGAATGCCCCCATCACAGACTTCTACTCCAGCAGTGTGACTAGGCAACGTC-CCC 4311
QY 511 CCCAGAACTCCCTGGGCGAGGCGAGCTCGGGTGAAGGGTGAAGTGGAGGAGACCCATGGCG 570

Db 4312 CCCAGAACTCCCTCGGGCAGAGCCAGCTCGGGTGAGGGGTAGTGGAGGAGACCCATGGCG 4371
Qy 571 GACAATCACTCTTTCTGCTCTCAGGACCCCGAGGTCTGACTTAGTGGGACCTGACCACT 630
Db 4372 GACAATCACTCTCTGCTCTCAGGACCCCGAGGTCTGACTTAGTGGGACCTGACCACT 4431
Qy 631 TTGCTCTTGGTTCCAGTTTGGATTAATTTCTGAGATTTTGGAGCTCAGTCCAGGTCCTC 690
Db 4432 TTGCTCTTGGTTCCAGTTTGGATTAATTTCTGAGATTTTGGAGCTCAGTCCAGGTCCTC 4491
Qy 691 CCCCACTGGATGGTCTGCTGCTGGAACCTTGTAAACCAACATGTGGGTAACCTGGGA 750
Db 4492 CCCCACTGGATGGTCTGCTGCTGGAACCTTGTAAACCAACATGTGGGTAACCTGGGA 4551
Qy 751 ATAAATGAAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCAATTCCTGCTT 810
Db 4552 ATAAATGAAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCAATTCCTGCTT 4611
Qy 811 AATGGTAATGACAAGTGTACCCCTGAGCCCGCAGGCCAACCCATCCCGAGTTGAGCCT 870
Db 4612 AATGGTAATGACAAGTGTACCCCTGAGCCCGCAGGCCAACCCATCCCGAGTTGAGCCT 4671
Qy 871 TATAGGTCAGTAGCTCTCCACATGAAGTCCCTCTCACTCACCACCTGTGAGGAGGAG 930
Db 4672 TATAGGTCAGTAGCTCTCCACATGAAGTCCCTCTCACTCACCACCTGTGAGGAGGAG 4731
Qy 931 GTGGTCATAGATCAGGATCTATGGCCCTTGGCCCGAGCCCAACCCCTTCCCTT -ATC 989
Db 4732 GTGGTCATAGATCAGGATCTATGGCCCTTGGCCCGAGCCCAACCCCTTCCCTTAAATC 4791
Qy 990 CTGCCACTGTCAATGCTACCTTTCCTATCTCTTCCCTCATCATCTCTGTGTGGGCATGA 1049
Db 4792 CTGCCACTGTCAATGCTACCTTTCCTATCTCTTCCCTCATCATCTCTGTGTGGGCATGA 4851
Qy 1050 GAGGTGGTATCTCAGAAATGCTTGGAGTCAAGATTAAGATTAAGTGGAT 1109
Db 4852 GAGGTGGTATCTCAGAAATGCTTGGAGTCAAGATTAAGATTAAGTGGAT 4911
Qy 1110 GCTGATCCTCTTTTAAACCCCAAGATCAATCAAAAT -CCAGATGCTGGTCTTATTC 1168
Db 4912 GCTGATCCTCTTTTAAACCCCAAGATCAATCAAAATCCCGAGTCTCTATTC 4971
Qy 1169 CCATGAAAAGTCTCATGACATATTGAGAAGACCTACTTACAAAGTGCATATATGCA 1228
Db 4972 CCATGAAAAGTCTCATGACATATTGAGAAGACCTACTTACAAAGTGCATATATGCA 5031
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Db 5152 CTGTTAATTTATCTGATTTCTTAAATTTTCTACAATGAAGATGAATCTTGTATPAAA 5211
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Qy 1469 CCTCCAAATCCCGAGATGAATCAAAATGAATCGAGCTCTGCTCTGGTTGGTTGTA 1528
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Qy 1529 GTAGTATCAGGAAAAGATCTCAGCAAGCCACTCAGGAGGAGGCTGTGCTGAGTTGT 1588
Db 5331 GTAGTATCAGGAAAAGATCTCAGCAAGCCACTCAGGAGGAGGCTGTGATGAGTTGT 5390
Qy 1589 GTGGCTGGATCTCTGGTGAAGAACTTAAGAACAAATCATCTGGAATTTCTTCTCT 1648
Db 5391 GTGGCTGGATCTCTGGTGAAGAACTTAAGAACAAATCATCTGGAATTTCTTCTCT 5450

RESULT 15

US-09-457-626-7
; Sequence 7, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/457,626
; EARLIER FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
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; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 5751
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(5751)
; OTHER INFORMATION: n = A,T,C or G
US-09-457-626-7

Query Match 63.1%; Score 1616.6; DB 3; Length 5751;
Best Local Similarity 98.9%; Pred. No. 0;

Matches 1663; Conservative 5; Mismatches 9; Indels 4; Gaps 4;			
QY	271	AGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAAAGGAATCCAAAGAGCTTCACTCTCT	330
Db	4073	AGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAAAGGAATCCAAAGAGCTTCACTCTCT	4132
QY	331	ACGGGGGACATGGGCTCACCTCCAGCTTCGAGTCCGGCTGCTACCCGGGCTGGTTCC	390
Db	4133	ACGGGGGACATGGGCTCACCTCCAGCTTCGAGTCCGGCTGCTACCCGGGCTGGTTCC	4192
QY	391	TGTGACGGTGGCTGAAGCCGATCAGCTGTGAGCTCACCCAGCTTCCCGAGAAATGGTG	450
Db	4193	TGTGACGGTGGCTGAAGCCGATCAGCTGTGAGCTCACCCAGCTTCCCGAGAAATGGTG	4252
QY	451	GTTGGAATCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGCAACGTCCTCC	510
Db	4253	GCTGGAATCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGCAACGTTG-CCT	4311
QY	511	CCAGAACTCCCTGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG	570
Db	4312	CCAGAACTCCCTGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG	4371
QY	571	GACAACTCACTTTCTGTCTCTCAGGACCCCGAGTCTGACTTAGTGGGCACCTGACCACT	630
Db	4372	GACAACTCACTTCTGTCTCTCAGGACCCCGAGTCTGACTTAGTGGGCACCTGACCACT	4431
QY	631	TTGTCTTCTGGTCCCGAGTTTGCATAAAATCTGAGATTTGGAGCTCAGTCCAGGGTCTTC	690
Db	4432	TTGTCTTCTGGTCCCGAGTTTGCATAAAATCTGAGATTTGGAGCTCAGTCCAGGGTCTTC	4491
QY	691	CCCACTGATGGTGTCTACTGTGTGGAACTTGTGAAACCATGTGGGGTAAACTGGGA	750
Db	4492	CCCACTGATGGTGTCTACTGTGTGGAACTTGTGAAACCATGTGGGGTAAACTGGGA	4551
QY	751	ATAACATGAAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGCTT	810
Db	4552	ATAACATGAAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGCTT	4611
QY	811	AATGGTAACTGACAAAGTGTATACCTTGAGCCCGCAGGCCAACCCATCCCGAGTGTAGCCT	870
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QY	871	TATAGGTCAGTAGTCTCCACATGAGTCTCTCACTCACCACATGTGCAGGAGGGAG	930
Db	4672	TATAGGTCAGTAGTCTCCACATGAGTCTCTCACTCACCACATGTGCAGGAGGGAG	4731
QY	931	GTGGTCATAGATCAGGGATCTATGGCCTTGSCCCAGCCACCCCTTCCCTTT-ATC	989
Db	4732	GTGGTCATAGATCAGGGATCTATGGCCTTGSCCCAGCCACCCCTTCCCTTTAATC	4791
QY	990	CTGCCACTGTCTATGCTACCTTTCTCTATCTTCTCCCTCATCTTTGTGGGCATGA	1049
Db	4792	CTGCCACTGTCTATGCTACCTTTCTCTATCTTCTCCCTCATCTTTGTGGGCATGA	4851
QY	1050	GGAGTGGTGTGTGAGAAAGAAATGGTTCGAGCTCAGAAAGATAAAGATAAGTGGGTAT	1109
Db	4852	GGAGTGGTGTGTGAGAAAGAAATGGTTCGAGCTCAGAAAGATAAAGATAAGTGGGTAT	4911
QY	1110	GCTGATCTCTTTTAAAAACCAAGTACATAACAAAT-CCAGATGCTGGTCTCTATTTC	1168
Db	4912	GCTGATCTCTTTTAAAAACCAAGTACATAACAAATCCAGATGCTGGTCTCTATTTC	4971
QY	1169	CCATGAAAAGTGTCTCATGACATATTGAGAAGACCTACTTACAAAGTGGCATATATTGCA	1228
Db	4972	CCATGAAAAGTGTCTCATGACATATTGAGAAGACCTACTTACAAAGTGGCATATATTGCA	5031
QY	1229	ATTTATTTTAAATTAAGAATACCTATTTATATATTCTTTATAGAAAAAGTCTGGAAGA	1288
Db	5032	ATTTATTTTAAATTAAGAATACCTATTTATATATTCTTTATAGAAAAAGTCTGGAAGA	5091
QY	1289	GTTTACTTCAATGTAGCAATGTGAGGGTGGGCGAGTATAGGTGATTTTCTTTTAATT	1348
Db	5092	GTTTACTTCAATGTAGCAATGTGAGGGTGGGCGAGTATAGGTGATTTTCTTTTAATT	5151

Search completed: March 13, 2005, 18:22:11
Job time : 495.866 secs

QY	1349	CTGTTAAATTTATCTGTATTTTCTTAATTTTCTAATGAAGATGAATTCCTTGTATAAAA	1408
Db	5152	CTGTTAAATTTATCTGTATTTTCTTAATTTTCTAATGAAGATGAATTCCTTGTATAAAA	5211
QY	1409	ATAAGAAAGAAATTAATCTTTCAGGTAAAGCAGAGAGACATCATCTCTGATTTCTCAG	1468
Db	5212	ATAAGAAAGAAATTAATCTTTCAGGTAAAGCAGAGAGACATCATCTCTGATKG-CCTCAG	5270
QY	1469	CCTCAAATTTCCCCAGAGTAAATTTCAAATTTGAATCGAGCTCTGCTCTGGTTGGTTGTA	1528
Db	5271	CCTCCACTTTCCCCAGAGTAAATTTCAAATTTGAATCGAGCTCTGCTCTGGTTGGTTGTA	5330
QY	1529	GTAGTGTATCAGAAACAGATCTCAGAAAGCCACTGAGGAGGAGGCTGTGAGTTTGT	1588
Db	5331	GTAGTGTATCAGAAACAGATCTCAGAAAGCCACTGAGGAGGAGGCTGTGATGAGTTTGT	5390
QY	1589	GTGGCTGGAACTCTCTGGGTAAAGAACTTAAAGAAACAAATCATCTGGTAAATTTCTTCT	1648
Db	5391	GTGGCTGGAACTCTCTGGGTAAAGAACTTAAAGAAACAAATCATCTGGTAAATTTCTTCT	5450
QY	1649	AGAAGGATCACAGCCCCCTGGGATTTCAAAGGCAATTGGATCCAGTCTCTAAGAAAGGCTGCTG	1708
Db	5451	AGAAGGATCACAGCCCCCTGGGATTTCAAAGGCAATTGGATCCAGTCTCTAAGAAAGGCTGCTG	5510
QY	1709	TACTGGTTGAATTTGTGTCCTTCAAAATTCACATCCTTCTTGGAAATCTCAGTCTGTGAGT	1768
Db	5511	TACTGGTTGAATTTGTGTCCTTCAAAATTCACATCCTTCTTGGAAATCTCAGTCTGTGAGT	5570
QY	1769	TTATTTGGAGATAAGGTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTATCTGGATGAA	1828
Db	5571	TTATTTGGAGATAAGGTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTATCTGGATGAA	5630
QY	1829	GGTAGACCTAAATTTCAATATGACTGGTTTCTTGTATGAAAAGAGGAGACACAGAGACA	1888
Db	5631	GGTAGACCTAAATTTCAATATGACTGGTTTCTTGTATGAAAAGAGGAGACACAGAGACA	5690
QY	1889	GAGGAGACGCGGGGAAGACTATGTAAAGATGAAGCAGAGATCGGAGTTTTCAGGCCACA	1948
Db	5691	GAGGAGACGCGGGGAAGACTATGTAAAGATGAAGCAGAGATCGGAGTTTTCAGGCCACA	5750
QY	1949	A 1949	
Db	5751	A 5751	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 10:45:20 ; Search time 22.9062 Seconds
(without alignments)
10854.228 Million cell updates/sec

Title: US-09-617-720A-3

Perfect score: 42

Sequence: 1 aagggaaggaggaggaagga.....gagtgagaaggagtgaaa 42

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	42	100.0	42	5	Aaf27923 Human IL-
2	42	100.0	73	5	Aaf27926 Interleuk
3	42	100.0	6540	5	Aaf27950 Interleuk
4	42	100.0	7605	2	Aaz30053 DNA encod
5	42	100.0	7605	4	Aaf31356 Extension
6	42	100.0	7605	8	Abz77451 Extended
7	33	78.6	446	2	Aaq95200 Simple ta
8	32	76.2	110000	13	ABD32923_6
9	31.4	74.8	4579	12	ADJ75968 Marker ge
10	31.4	74.8	165156	13	ADJ75968 Human aut
11	31.4	74.8	335199	10	Adc24703 Human wil
12	30.8	73.3	52661	9	Ada02876 Human DPT
13	30.8	73.3	52661	10	Adb72614 Human DPT
14	30.8	73.3	52661	10	Adc85355 Mouse Dpt
15	30.8	73.3	52661	12	ADW74471 Human car
16	30.8	73.3	59588	10	Adc87426 Human GPC
17	30.8	73.3	74822	6	ABT10752 Human bre
18	30.4	72.4	3973	6	AB132170 Human imm
19	29.8	71.0	496	6	ABK88541 Human cho
20	29.8	71.0	867	3	AAZ98056 Human sec

C 21	29.8	71.0	867	4	AAD11669	Ad11669 Human sec
C 22	29.8	71.0	867	6	ABK69765	Abk69765 Human sec
C 23	29.8	71.0	867	8	ADA39774	Ada39774 Human sec
C 24	29.8	71.0	867	8	ACC50425	Acc50425 Human sec
C 25	29.8	71.0	867	8	ABZ71239	Abz71239 Human sec
C 26	29.8	71.0	867	9	ADB91132	Adb91132 Human sec
C 27	29.8	71.0	867	10	ADC73483	Adc73483 Human sec
C 28	29.8	71.0	867	10	ADA55964	Ada55964 Gene enco
C 29	29.8	71.0	2777	8	AH332536	Aah332536 Human sec
C 30	29.8	71.0	2777	4	ADA39721	Ada39721 Human sec
C 31	29.8	71.0	2777	8	ACC50392	Acc50392 Human sec
C 32	29.8	71.0	2777	10	ADA55915	Ada55915 Gene enco
C 33	29.8	71.0	12141	4	AAF62854	Aaf62854 Mouse PEP
C 34	29.8	71.0	12141	12	ADP18732	Adp18732 Mouse lip
C 35	29.8	71.0	21777	4	AAK74096	Aak74096 Human imm
C 36	29.8	71.0	28729	11	ACN43928	Acn43928 Mouse gen
C 37	29.8	71.0	41966	11	ACN45050	Acn45050 Human gen
C 38	29.8	71.0	57082	12	ADP84151	Adp84151 Human CAL
C 39	29.8	71.0	96589	9	AAU57700	Aal57700 Mouse pro
C 40	29.8	71.0	96592	9	ADA02669	Ada02669 Mouse Prl
C 41	29.8	71.0	96592	10	ADB72407	Adb72407 Mouse Prl
C 42	29.8	71.0	96592	10	ADE95917	Ade95917 Mouse Prl
C 43	29.8	71.0	97658	8	ABO83210_3	Continuation (4 of
C 44	29.8	71.0	110000	13	ABD32594_3	Continuation (4 of
C 45	29.8	71.0	117962	8	AAD54480	Ad54480 Human CIP

ALIGNMENTS

RESULT 1
AAF27923
ID AAF27923 standard; cDNA; 42 BP.
XX
AC AAF27923;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human IL-IL1 coding sequence 5' end #2.
XX
KW Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
KW osteoporosis; systemic lupus erythematosus; ss.
XX
OS Homo sapiens.
XX
PN WO200105974-A2.
XX
PD 25-JAN-2001.
XX
PP 17-JUL-2000; 2000WO-US019508.
XX
PR 16-JUL-1999; 99US-0144298P.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Nicklin M, Barton J;
XX
DR WPI; 2001-091974/10.
XX
PT Nucleic acids encoding human and murine interleukin-IL1 polypeptides
PT useful for controlling inflammatory processes.
XX
PS Claim 21; Fig 1; 150pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human and murine interleukin-IL1 (IL-IL1) proteins. The IL-IL1 gene is
CC located between the IL-1beta and IL-1receptor genes at human chromosome
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
CC of heart disease, cancer and inflammatory diseases such as rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,

DE	Extension of genomic clone B2HFLS20W.
KX	interleukin; IL-1 receptor; cancer; inflammation; ds.
XX	
OS	Homo sapiens.
XX	
XX	WO200102571-A2.
PN	
XX	
PD	11-JAN-2001.
XX	
PF	07-JUL-2000; 2000WO-US018710.
XX	
PR	07-JUL-1999; 99US-00348942.
PR	13-OCT-1999; 99US-00417455.
PR	08-DEC-1999; 99US-00457626.
PR	10-MAR-2000; 2000US-00523552.
PR	22-MAY-2000; 2000US-00576008.
XX	
PA	(HYSE-) HYSQ INC.
XX	
PI	Ford J, Pace A;
XX	
DR	WPI; 2001-071592/08.
XX	
PT	Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist proteins (referred as IL-1Hyl), useful in the treatment of cancer, e.g. breast adenocarcinoma and brain tumors, and an inflammatory disease mediated by IL-18.
PT	
PT	
PS	Disclosure; Fig 10; 179pp; English.
XX	
CC	The present invention relates to interleukin (IL)-1 receptor antagonist proteins. IL-1Hyl is useful for treating cancer, an inflammatory disease mediated by IL-18, inflammation resulting from infection or allergic reactions, and inflammation associated with chronic bronchitis, arthritis, diabetes or endothermia
XX	
SQ	Sequence 7605 BP; 2079 A; 1647 C; 1865 G; 2009 T; 0 U; 5 Other;
	Query Match 100.0%; Score 42; DB 4; Length 7605;
	Best Local Similarity 100.0%; Pred. No. 0.0015;
	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AAGCAAGGGGGAAGGAAAGGAGTGAAGGAAGGAGTGAAA 42 Db 1339 AAGCAAGGGGGAAGGAAAGGAGTGAAGGAAGGAGTGAAA 1380
/	
RESULT 6	
ID ABZ77451	
ID ABZ77451 standard; cDNA; 7605 BP.	
XX	
AC ABZ77451;	
XX	
DT 28-MAY-2003 (first entry)	
XX	
DE Extended genomic DNA sequence of a human Interleukin-1Hyl (IL-1Hyl).	
XX	
KW Interleukin-1Hyl; IL-1Hyl; B-cell proliferation; B-cell activation; KW K cell differentiation; B-cell-related disorder; lymphoma; leukemia; KW myeloma; infection; autoimmune disease; allergy; asthma; KW allergic rhinitis; IgA production; ss.	
OS	Homo sapiens.
XX	
PN WO2003010291-A2.	
XX	
PD 06-FEB-2003.	
XX	
PF 25-JUL-2002; 2002WO-US023845.	
XX	
PR 25-JUL-2001; 2001US-0307754P.	
PR 29-NOV-2001; 2001US-0334568P.	

Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Example 11; SEQ ID NO 1220; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present invention is used in the exemplification of the present invention.

Sequence 4579 BP; 1124 A; 1151 C; 1149 G; 1155 T; 0 U; 0 Other;

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every Match      74.8%; Score 31.4; DB 12; Length 4579;
Best Local Similarity 85.4%; Pred. No. 2.3;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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1 AAGGAAGGAGGGAGAGGGAAGGAGTGAAGGAAGGAGTAA 41
|||||
2753 AAGGAAGGAGGGAGGGAAGGGAAGGGAAGGAAGGAAGGAA 2713

LT 10

6459

AD536459 standard; DNA; 165156 BP.

ADS36459:

16-DEC-2004 (first entry)

Human autoimmune disease-related genomic DNA sequence - SEO ID 1673.

single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; thyroiditis; celiac disease; pernicious anaemia; asthma; glomerulonephritis; Grave's disease; myocarditis; Sjogren's syndrome; primary systemic vasculitis; de.

Homo sapiens.

WQ2004083403-A2

30-SEP-2004

18-MAR-2004: 2004WO-IIS008461

18-MAR-2003; 2003US-0455444P.
25-APR-2003; 2003US-0465241P.
{APPL-} APPLERA CORP.

Cargill M, Begovich AB, Alexander HC;

WPI; 2004-728480/71.

New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.

Claim 16: SEO ID NO 1673; 123pp; English.

The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for diagnosing and treating autoimmune diseases, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease, myocarditis, Sjogren's disease, or primary systemic vasculitis. The present nucleic acid represents a human autoimmune disease-related genomic DNA sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the WIPO website.

Sequence 165156 BP: 45717 A: 35582 C: 35601 G: 47895 T: 0 U: 361 Other:

74.88: Score 31.4: DB 13: Length 165156:

1st Local Similarity	85.4%	Pred. No. 2.9;	
Matches	35;	Conservative	0;
Mismatches	6;	Indels	0;
Gaps	0;		

1 AAGGAAGGAGGGAGAAAGGGAAGGAGTGAACGAACGAGTGAA 41

80763 AAGGAAGGAAGGAGGGAGGGAGGGAAGGAAGGAAGGAA 80803

It is

4703/c
ADC24703 standard; DNA; 335199 BP.

ADC24703:

18-DEC-2003 (first entry)

Human wild type HNT.4Y genomic sequence.

ds; nootropic; neuroleptic; tranquilizer; gene therapy; synaptogenesis; mutation; neurological disease; mental disorder; psychiatric illness; autism; Asperger syndrome; schizophrenia; attention deficit hyperactivity disorder.

Homo sapiens.

Key	Location/Qualifiers
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intron
10299. .1084999
/transcript= ID

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exon
108500. .109001

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/number= ?
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int rpn
/number= 2
109002 205868

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1002072: .dta/*

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number= 2

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CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;
Query Match 73.3%; Score 30.8; DB 9; Length 52661;
Best Local Similarity 83.3%; Pred. No. 4.1;
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGGAAGGAGGAGAAGGGAAGGAGTGAAGGAGGAGTGAAA 42
| | | | | | | | | | | | | | | | | | | | |
Db 13858 AGCGAGGGAGGAGGAGGAGGATTGAAGGAAGGAGAAA 13899

RESULT 13
ADB72614
ID ADB72614 standard; DNA; 52661 BP.
XX
AC ADB72614;
XX
DT 04-DEC-2003 (first entry)
DE Human DPT gene.
XX
KW human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.
OS Homo sapiens.
XX
PN WO2003008583-A2.
XX
PP 30-JAN-2003.
XX
XX 26-DEC-2001; 2001WO-US051291.
XX
PR 02-MAR-2001; 2001US-00798586.
PR 23-OCT-2001; 2001US-00004113.
PR 08-NOV-2001; 2001US-00052482.
PR 30-NOV-2001; 2001US-00997722.
PR 20-DEC-2001; 2001US-00034650.
XX
PA (SAGR-) SAGES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX
PS WPI; 2003-239337/23.
XX
DR New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
PT Claim 1; SEQ ID NO 442; 2304pp; English.
XX
PS The invention relates to a novel recombinant nucleic acid comprising a
XX nucleotide sequence selected from any of the 660 sequences fully defined
XX in the specification. A polynucleotide of the invention has cytosolic
XX activity, and may have a use in gene therapy, or in a vaccine. The
XX recombinant nucleic acids and polypeptides are useful for treating
XX carcinomas, e.g. lymphomas, cancers, neoplasms, adenocarcinoma, and
XX sarcomas. The present sequence represents a human gene of the invention.
XX
SQ Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;
Query Match 73.3%; Score 30.8; DB 10; Length 52661;
Best Local Similarity 83.3%; Pred. No. 4.1;
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGGAAGGAGGAGAAGGGAAGGAGTGAAGGAGGAGTGAAA 42
| | | | | | | | | | | | | | | | | | | | |
Db 13858 AGCGAGGGAGGAGGAGGAGGATTGAAGGAAGGAGAAA 13899

RESULT 14
ADC85355

Search completed: March 13, 2005, 12:34:23
Job time : 29.5729 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:14:57 ; Search time 11331.9 Seconds
(without alignments)
10959.418 Million cell updates/sec

Title: US-09-617-720A-1
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_to.*
- 11: gb_ets.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2514.2	98.1	2598	6	AX092420 Sequence
5	2514.2	98.1	2598	6	AX454730 Sequence
6	2514.2	98.1	2598	6	AX491208 Sequence
7	2514.2	98.1	2598	9	AX359117 Homo sapi
8	2512	98.0	2692	9	BC024747 Homo sapi
9	2504.2	97.7	2701	6	C0722801 Sequence
10	2488.4	97.1	2648	6	BD211435 A novel i
11	2488.4	97.1	2648	6	AR181995 Sequence
12	2488.4	97.1	2648	6	AR221129 Sequence
13	2488.4	97.1	2648	6	AR302957 Sequence
14	2488.4	97.1	2648	6	AX069309 Sequence
15	2488.4	97.1	2720	9	AF186094 Homo sapi
16	2488.4	97.1	2720	9	AF186094 Homo sapi
17	2235.6	87.2	6540	6	AX080431 Sequence
18	2229.2	87.0	197308	9	HS24271338
19	2220.4	86.6	7604	9	AF216693 Homo sapi

20	2220.4	86.6	7605	6	BD211437	BD211437 A novel i
21	2220.4	86.6	7605	6	AR181997	AR181997 Sequence
22	2220.4	86.6	7605	6	AR221131	AR221131 Sequence
23	2220.4	86.6	7605	6	AR302959	AR302959 Sequence
24	2220.4	86.6	7605	6	AX069311	AX069311 Sequence
25	1835	71.6	1866	6	BD157091	BD157091 Primer fo
26	1835	71.6	1866	6	AX878219	AX878219 Sequence
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36	1195.2	46.6	1282	6	AR221128	AR221128 Sequence
37	1195.2	46.6	1282	6	AR302956	AR302956 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 1 from Patent WO0105974.
ACCESSION AX080389
VERSION AX080389.1 GI:13159840
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nicklin,M. and Barton,J.
TITLE The il-111 gene and polypeptide products
JOURNAL Patent: WO 0105974-A 1 25-JAN-2001;
Interleukin Genetics, Inc. (US)
FEATURES
source location/Qualifiers
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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	1201	ACCTACTTACAAAGTGGCATATATGCAATTTATTTAAAGTACCTATTTATAT	1260	QY	2281	GGTTATAAAGACATGCGAGCTTCTACTTGGCCCTCTCTCTGCGCCACCCCGCCCC	2340
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RESULT 2
LOCUS   HSA242738                2604 bp    mRNA    linear    PRI 18-APR-2002
DEFINITION Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L1 gene)
transcript 2.
ACCESSION AJ242738
VERSION   AJ242738.1 GI:6165335
KEYWORDS IL1L1 gene; interleukin-1-like protein 1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Barton,J.L., Herbst,R., Bosio,D., Higgins,L. and Nicklin,M.J.
TITLE     A tissue specific IL-1 receptor antagonist homolog from the IL-1
           cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
JOURNAL   Eur. J. Immunol. 30 (11), 3299-3308 (2000)
MEDLINE   20545212
PUBMED    11093146
REFERENCE 2 (bases 1 to 2504)
AUTHORS   Nicklin,M.J.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and
           Genetic Medicine, University of Sheffield, Royal Hallamshire
           Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
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Matches 2561; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1980 TCAGAAGCTTGAAGAGGCAAGAGAAATTTCTTCCCTAGAGCTTTAGAGGATTAACGGC 2039
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RESULT 3
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Homo sapiens mRNA for interleukin-1-like protein-1 (IL1L1 gene),
transcript 1.
ACCESSION
AJ242737
VERSION
AJ242737.1
GI:6165333
KEYWORDS
IL1L1 gene; interleukin-1-like protein-1.
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS
Barton,J.L., Herbst,R., Bosio,S.D., Higgins,L. and Nicklin,M.J.
TITLE
A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
JOURNAL
Eur. J. Immunol. 30 (11), 3299-3308 (2000)
MEDLINE
20545212
PUBMED
11093146
REFERENCE
2 (bases 1 to 2613)
AUTHORS
Nicklin,M.J.
TITLE
Direct Submission
JOURNAL
Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
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DEFINITION Sequence 151 from Patent WO0116318.
ACCESSION AX092420
VERSION AX092420.1 GI:13444524
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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Genentech, Inc. (US)
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
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Db 98 TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACAGCTTCTAGCTGGAGGC 157
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LOCUS Sequence 315 from Patent WO0208284.
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ACCESSION AX454730
VERSION AX454730.1 GI:21713989
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 315 31-JAN-2002;
Gentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES
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Qy 1500 ATCCAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTATGATCAGGAAACAGATCTCAGCAAGC 1559
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Qy 1560 CACTCAGAGGAGGCTGTGTGAGTTGTGTGGCTGGAATCTCTGGGTAAGGAATCTTAA 1619
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Qy 1620 GAACAAAATCATCTGGTAAATTTCTCTAGAAGGATCAGAGCCCTGGGATTCAGAGC 1679
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Qy 1800 TTAGTTAAGACNAGTCTATGATGAAGTGTAGACCTTAAATTTCAATATGATCTGTTTCC 1859
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Qy 1860 TTGTATGAAAAAGGAGAGACACAGACAGAGGAGACCGGGGAGAGATATGTAAGATG 1919
Db 1897 TTGTATGAAAAAGGAGAGACACAGACAGAGGAGACCGGGGAGAGATATGTAAGATG 1956
Qy 1920 AAGCAGAGATCGAGTTTTCAGCCCAAGCTAAGAAACACCAAGGATTTGGCAACCA 1979
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Qy 1980 TCAGAGCTTGAAGAGGCAAAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGCG 2039
Db 2017 TCAGAGCTTGAAGAGGCAAAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGCG 2076
Qy 2040 TCTGCTGAAACCTTAAATCTCAGACTTCCAGCTCTCTGAACGAAAGAAATAAATTTCCG 2099
Db 2077 TCTGCTGAAACCTTAAATCTCAGACTTCCAGCTCTCTGAACGAAAGAAATAAATTTCCG 2136
Qy 2100 CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAACTAATACAGTGT 2159
Db 2137 CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAACTAATACAGTGT 2196
Qy 2160 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCACAAATGTACA 2219
Db 2197 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCACAAATGTACA 2256
Qy 2220 AAGTTGTCTTTGTGACCCCAATAAGATATGCGAGAGTGTGATGCGATGCCACTTCCAGATT 2279
Db 2257 AAGTTGTCTTTGTGACCCCAATAAGATATGCGAGAGTGTGATGCGATGCCACTTCCAGATT 2315
Qy 2280 AGTTTAAAGACACATGCGAGCTTCTACTTGAAGCCTCTCTCTGCGCAACCCACCGCC 2339
Db 2316 AGTTTAAAGACACATGCGAGCTTCTACTTGAAGCCTCTCTCTGCGCAACCCACCGCC 2375
Qy 2340 CAATCTATCTTGGCTCAGTCCGCTCTGGGGGAAAGTAGTGTCCATGTATGAGAGGCTTA 2399
Db 2376 CAATCTATCTTGGCTCAGTCCGCTCTGGGGGAAAGTAGTGTCCATGTATGAGAGGCTTA 2435
Qy 2400 TAAAGAGACTTACGTGGTAAAAATAAGAGTCTCTGCGCCACAGCCACATTTAGTACCTTA 2459
Db 2436 TAAAGAGACTTACGTGGTAAAAATAAGAGTCTCTGCGCCACAGCCACATTTAGTACCTTA 2495

Db	1597	C	ACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGCTGGAATCTCTGGGTAAAGAACTTAAA	1656
Qy	1620	G	AACAAAAATCACTCTGTAATCTTTTCTTAGAGGATCACAGCCCTCGGATTCGAAGC	1679
Db	1657	G	AACAAAAATCACTCTGTAATCTTTTCTTAGAGGATCACAGCCCTCGGATTCGAAGC	1716
Qy	1680	A	TTGGATCCAGTCTCTAAGAGGCTGCTGTAATCTTTGTTGAAATGTGTCCCTCAAATCA	1739
Db	1717	A	TTGGATCCAGTCTCTAAGAGGCTGCTGTAATCTTTGTTGAAATGTGTCCCTCAAATCA	1776
Qy	1740	C	ATCTTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG	1799
Db	1777	C	ATCTTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG	1836
Qy	1800	T	TAGTTAAGACAAGGTCTATCTGGATCAAGGTAGACTAAATCAATATGACTGGTTTCC	1859
Db	1837	T	TAGTTAAGACAAGGTCTATCTGGATCAAGGTAGACTAAATCAATATGACTGGTTTCC	1896
Qy	1860	T	TGATGAAAAAGGAGAGACACAGACACAGAGACGCGGGGAAGACTATGTAAAGATG	1919
Db	1897	T	TGATGAAAAAGGAGAGACACAGACACAGAGACGCGGGGAAGACTATGTAAAGATG	1956
Qy	1920	A	AGCAGAGATCGAGTTTTGCACCAACAAGTAAGAAAACCAAGATTTGGGAACCA	1979
Db	1957	A	AGCAGAGATCGAGTTTTGCACCAACAAGTAAGAAAACCAAGATTTGGGAACCA	2016
Qy	1980	T	CAGAGCTTGAAGAGCAAGAAAGAAATCTTCCCTAGAGGCTTTAGAGGATAACGGC	2039
Db	2017	T	CAGAGCTTGAAGAGCAAGAAAGAAATCTTCCCTAGAGGCTTTAGAGGATAACGGC	2076
Qy	2040	T	CTGCTGAAACCTTAATCTCAGACTTCCAGCCTCTGAAAGAAAGAAATAAATTCGG	2099
Db	2077	T	CTGCTGAAACCTTAATCTCAGACTTCCAGCCTCTGAAAGAAAGAAATAAATTCGG	2136
Qy	2100	C	TGTTTTAAGCCACAAGATAATTTGTTACAGAGCTCTAGGAACTAATACAGTGTCT	2159
Db	2137	C	TGTTTTAAGCCACAAGATAATTTGTTACAGAGCTCTAGGAACTAATACAGTGTCT	2196
Qy	2160	A	AATGATCCCTGTCTCTCGTGTATCATCTCTGTGTGTCCTCCCAATGTACCA	2219
Db	2197	A	AATGATCCCTGTCTCTCGTGTATCATCTCTGTGTGTCCTCCCAATGTACCA	2256
Qy	2220	A	AGTTGTCTTTGTGACCCAAATAGAAATATGGCAGAAGTGATGGCATGCCATCCAGATT	2279
Db	2257	A	AGTTGTCTTTGTGA-CCAAATAGAAATATGGCAGAAGTGATGGCATGCCATCCAGATT	2315
Qy	2280	A	GGTTATAAAGACACTGAGCTTCTACTTGAGCCCTCTCTCTGCGCACCCACGCCCC	2339
Db	2316	A	GGTTATAAAGACACTGAGCTTCTACTTGAGCCCTCTCTCTGCGCACCCACGCCCC	2375
Qy	2340	C	AATCTAATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCGCATGTCTATGACAGGCTA	2399
Db	2376	C	AATCTAATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCGCATGTCTATGACAGGCTA	2435
Qy	2400	T	AAAGAGACTTACGTGGTAAAAAATGAAGTCTCTCTGCCACAGCCACATTAAGTGAACCTA	2459
Db	2436	T	AAAGAGACTTACGTGGTAAAAAATGAAGTCTCTCTGCCACAGCCACATTAAGTGAACCTA	2495
Qy	2460	G	AAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTGTCTCAGTTTGTCT	2519
Db	2496	G	AAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTGTCTCAGTTTGTCT	2555
Qy	2520	A	ACTTGTATGAGCAATAGATAAATATATGCAGAGAAAG	2562
Db	2556	A	ACTTGTATGAGCAATAGATAAATATATGCAGAGAAAG	2598

RESULT 7

AY359117

LOCUS

DEFINITION

ACCESSION

VERSION

AY359117

Homo sapiens clone DNA96787 ILH1Y1 (UNQ1896)

mRNA, complete cds.

AY359117

AY359117.1

GI:37183350

2598 bp

mRNA

linear

PRI 03-OCT-2003

QY 361 TCAGTCCGGCTGCTACCCGGGCTGGTTCCTGTGACCGTGCCTGAAGCGGATCAGCCTG 420
Db 398 TCAGTCCGGCTGCTACCCGGGCTGGTTCCTGTGACCGTGCCTGAAGCGGATCAGCCTG 457
QY 421 TCAGACTCACCCAGACTTCCCGAGAAATGGTGGTGGAAATGCCCCATCAGAGACTTCTACT 480
Db 458 TCAGACTCACCCAGACTTCCCGAGAAATGGTGGTGGAAATGCCCCATCAGAGACTTCTACT 517
QY 481 TCAGCAGTGTGA CTAGGCAJACGTGCCCCCCCCCCAGAACTCCCTGGGCGAGCCAGCTCGG 540
Db 518 TCAGCAGTGTGA CTAGGCAJACGTGCCCCCCCCCCAGAACTCCCTGGGCGAGCCAGCTCGG 576
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QY 601 CAGGCTGACTTAGTGGGCACTGACCACTTGTGTCTTCTGGTTCGCCAGTTTGCATAAAT 660
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QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCCCACTGGATGGTGTACTGTCTGGAAAC 720
Db 697 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCCCACTGGATGGTGTACTGTCTGGAAAC 756
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QY 781 GTGGGGAGTGTGGGAATCATTTCTGCTTAATGGTAACTGACAAGTGTACCTCGAGCC 840
Db 817 GTGGGGAGTGTGGGNATCATTTCTGCTTAATGGTAACTGACAAGTGTACCTCGAGCC 876
QY 841 CGCGAGGCCAACCCATCCCAGTTGAGCCCTTATAGGGTCAGTAGTCTCCACATGAAGTC 900
Db 877 CGCGAGGCCAACCCATCCCAGTTGAGCCCTTATAGGGTCAGTAGTCTCCACATGAAGTC 936
QY 901 CTCTCACTCACACTGTGACAGAGAGGAGGTGGTCAATAGATCAGGGATCATGGCCCT 960
Db 937 CTGTCACTCACACTGTGACAGAGAGGAGGTGGTCAATAGATCAGGGATCATGGCCCT 996
QY 961 TGGCCAGCCCAACCCCTTCCCTTT - ATCCTGCCACTGTCATATGCTACCTTTCCCTATC 1019
Db 997 TGGCCAGCCCAACCCCTTCCCTTTAATCTTGGCCACTGTGATATGCTACCTTTCCCTATC 1056
QY 1020 TCTTCCCTCATCTTGTGTGGGATGAGGAGGTGGTGTGTCAGAGAAATGGTTCCG 1079
Db 1057 TCTTCCCTCATCTTGTGTGGGATGAGGAGGTGGTGTGTCAGAGAAATGGCTCG 1116
QY 1080 AGCTCAGAAAGATAAAGATAAGTAGGGTATGCTGATCCCTTTTAAAAACCCCAAGATACA 1139
Db 1117 AGCTCAGAAAGATAAAGATAAGTAGGGTATGCTGATCCCTTTTAAAAACCCCAAGATACA 1176
QY 1140 ATCAAAATCCAGATGCTGCTCTATTCCCATGAAGAAGTGTCAATGACATATTGAGAA 1199
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QY 1620 GAACAAAATCATCTGGTAAATTTCTTCCCTAGAGGATCAGAGCCCTGGGATTCGAAGC 1679
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QY 1740 CATCTCTTTGGAATCTCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCGAGATGTAG 1799
Db 1777 CATCTCTTTGGAATCTCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCGAGATGTAG 1836
QY 1800 TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTTCAATATGACTGGTTTCC 1859
Db 1837 TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTTCAATATGACTGGTTTCC 1896
QY 1860 TTGTATGAAAAAGGAGAGGACACAGACACAGAGAGAGCGGGGGAAGACTATGTAAGAGATG 1919
Db 1897 TTGTATGAAAAAGGAGAGGACACAGACACAGAGAGAGCGGGGGAAGACTATGTAAGAGATG 1956
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QY 1980 TCAGAGCTTTGAAAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2039
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Db 2077 TCTGCTGAAACCTTAATCTCAGACTTCCAGCCTCTCGAAACGAAGAAGAAATAATTTTCGG 2136
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Db 2137 CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAAACTAATAACGTGCT 2196
QY 2160 AAAATGATCCCTGTCTCCTCGTGTTTACATTTCTGTGTGTCTCCCTCCACATGTACCA 2219
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Db 2257 AAGTTGTCTTTGTGA - CCAATAGAAATATGGCAGAGTGTATGGCATGCCACTTCCAAAGATT 2315
QY 2280 AGGTTATAAAGACACTGCACTTCTACTTGGCCCTCTCTCTGTCGCCACCCACGCCCC 2339
Db 2316 AGGTTATAAAGACACTGCACTTCTACTTGGCCCTCTCTCTGTCGCCACCCACGCCCC 2375
QY 2340 CAATCTATCTTGGTCACTCGCTCTGGGGGAGTAGCTGCCATGCTATGAGCAGGCTTA 2399
Db 2376 CAATCTATCTTGGTCACTCGCTCTGGGGGAGTAGCTGCCATGCTATGAGCAGGCTTA 2435
QY 2400 TAAAGAGACTTACGTGGTAAAAATGAAGTCTCTGCCCAACAGCCACATTTAGTGAACCTA 2459
Db 2436 TAAAGAGACTTACGTGGTAAAAATGAAGTCTCTGCCCAACAGCCACATTTAGTGAACCTA 2495
QY 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTTAAAGTGTCTCAGTTTGGTCT 2519
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTTAAAGTGTCTCAGTTTGGTCT 2555
QY 2520 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562

DB	2556	AACTTGTATGACGCAATAGATATAATAATATATGACAGAAAGAG	2598
RESULT 8	BC024747		
LOCUS			
DEFINITION	Homo sapiens interleukin 1 family, member 5 (delta), transcript variant 2, mRNA (cDNA clone MGC:29840 IMAGE:4996939), complete cds.		
ACCESSION	BC024747		
VERSION	BC024747.1	GI:19353229	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2692)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2692)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabs-x@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 42 Row: k Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894309. Location/Qualifiers 1. .2692 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:29840 IMAGE:4996939" /tissue_type="Placenta, Choriocarcinoma" /clone_lib="NIH_MGC_10"		
source			
gene	/lab_host="DH10B" /note="Vector: pCMV-SPORT6" 1. .2692 /gene="IL1F5" /note="synonyms: FIL1 (DELTA), FIL1D, IL1RP3, IL1HV1, FIL1, IL1L1, MGC29840" /db_xref="LocustID:26525" /db_xref="MIM:605507" 134. .601 /gene="IL1F5" /codon_start=1 /product="interleukin 1 family, member 5" /protein_id="AAH24747.1" /db_xref="GI:19353230" /db_xref="LocustID:26525" /db_xref="MIM:605507" /translation="MVLGALCFRMDKLSALKVLYLHNQLLAGLHAGKVIKGEISV VPRNLDAISPVILGVQSGQCLSCGVGDEPTLTLEPVNIMELYLGAKSKSTFFYR RDMGLTSSFSFAAYPGWFLCTVPEADQVRLTQIPENGGNAPITDFYFOCD"		
CDS	ORIGIN Query Match 98.0%; Score 2512; DB 9; Length 2692; Best Local Similarity 99.5%; Pred. No. 0; Matches 2551; Conservative 0; Mismatches 10; Indels 3; Gaps 3; QY 1 AGGGGAGTCTACACCTGTGAGCTCAAGATGTCCTGAGTGGGGCGCTGTGCTTCGAA 60 DB 105 AGGGGAGTCTACACCTGTGAGCTCAAGATGTCCTGAGTGGGGCGCTGTGCTTCGAA 164 QY 61 TGAAGGACTCGGATGAGAGTGGTCTTATCTGCATATATAACACGCTTCTAGCTCGAGGC 120 DB 165 TGAAGGACTCGGATGAGAGTGGTCTTATCTGCATATATAACACGCTTCTAGCTCGAGGC 224 QY 121 TGCAATGACGAGGAGTCAATTAAGTGAAGAGATCAGCGTGGTCCCAATCGTGGTGG 180 DB 225 TGCAATGACGAGGAGTCAATTAAGTGAAGAGATCAGCGTGGTCCCAATCGTGGTGG 284 QY 181 ATGCCAGCTGTGCCCGCTCATCTCTGGTGTCCAGGTGGAAGCAGCGCTGTCTATGTG 240 DB 285 ATGCCAGCTGTGCCCGCTCATCTCTGGTGTCCAGGTGGAAGCAGCGCTGTCTATGTG 344 QY 241 GGGTGGGCGAGGAGCGGCTCTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTG 300 DB 345 GGGTGGGCGAGGAGCGGCTCTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTG 404 QY 301 GTGCCAAGGAATCCAAAGAGCTTCACTTTACCGCGGGGACATGGGGCTCACTCCAGCT 360 DB 405 GTGCCAAGGAATCCAAAGAGCTTCACTTTACCGCGGGGACATGGGGCTCACTCCAGCT 464 QY 361 TCGAGTGGGCTGCTTACCGGGGCTGGTTCCTGTGCACGCTGCTGAAGCCGATCAGCGCTG 420 DB 465 TCGAGTGGGCTGCTTACCGGGGCTGGTTCCTGTGCACGCTGCTGAAGCCGATCAGCGCTG 524 QY 421 TCAGACTACCCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCGCATCAAGCTTCTACT 480 DB 525 TCAGACTACCCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCGCATCAAGCTTCTACT 584 QY 481 TCCAGCAGTGTCACTAGGGCAACGTCGCCCGCCCAAGACTCCCTGGGCGAGCGAGCTCGG 540 DB 585 TCCAGCAGTGTCACTAGGGCAACGTCGCCCGCCCAAGACTCCCTGGGCGAGCGAGCTCGG 643 QY 541 GTGAGGGGTGAGTGGAGGAGCCATGGCGGACAATCACTCTTTCTGTCTCTCAGGACCCC 600 DB 644 GTGAGGGGTGAGTGGAGGAGCCATGGCGGACAATCACTCTCTGTCTCTCAGGACCCC 703 QY 601 CAGGTCTGACTAGTGGGCACTGACCACTTTTCTTTGGTTCAGTTTCCAGTTTGCATAAAT 660 DB 704 CAGGTCTGACTAGTGGGCACTGACCACTTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 763 QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCGCCCACTGATGCTGTCTGTCTGTGGAAC 720 DB 764 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCGCCCACTGATGCTGTCTGTCTGTGGAAC 823		

QY 721 CTTGTAAACCACTGTGGGTAACCTGGGAATAACATGAAGAATTTCTGTGGGGTGG 780
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QY 961 TGGCCAGGCCACCCCTTCCCTTT - ATCTGCCACTGTCATATGCTACCTTTCTCTATC 1019
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QY 1320 TGGCAGTAGGTGATTTTCTTTTAAATCTGTTAAATTTATCTGTTATTTCTTAAATTTTC 1379
Db 1424 TGGCAGTAGGTGATTTTCTTTTAAATCTGTTAAATTTATCTGTTATTTCTTAAATTTTC 1483
QY 1380 TACAATGAAGATGAATTCCTTGTATATAAATAAGAAAAGAAATTAATCTTGAGGTAAGCA 1439
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TITLE Interleukin-1 receptor antagonist and recombinant production
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DEFINITION Sequence 6 from patent US 6426191.
ACCESSION AR221129
VERSION AR221129.1 GI:23328014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 2648)
AUTHORS Ford, J. and Pace, A.
TITLE Assays involving an IL-1 receptor antagonist
JOURNAL Patent: US 6426191-A 6 30-JUL-2002;
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LOCUS AR302957 2648 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6 from patent US 6541623.
ACCESSION AR302957
VERSION AR302957.1 GI:31691557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 2648)
Ford, J., Ho, A.S.Y. and Pace, A.
Interleukin-1 receptor antagonist and uses thereof
Patent: US 6541623-A 6 01-APR-2003;
Location/Qualifiers
1..2648
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AUTHORS
TITLE
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ORIGIN
Query Match 97.1%; Score 2488.4; DB 6; Length 2648;
Best Local Similarity 99.4%; Pred. No. 0;
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 ORGANISM
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 Ford J. and Pace A.
 A interleukin-1 receptor antagonist and uses thereof
 Patent: WO 0102571-A 6 11-JAN-2001;
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LOCUS AF186094

DEFINITION Homo sapiens interleukin-1 receptor antagonist homolog (IL1HV1)

ACCESSION AF186094

VERSION AF186094.1 GI:6049804

KEYWORDS mRNA, complete cds.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2720)

AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Drmanac,R. and Ford,J.E.

TITLE IL1HV1: A novel interleukin-1 receptor antagonist gene

JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)

MEDLINE 99443727

PUBMED 10512743

REFERENCE 2 (bases 1 to 2720)

AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Drmanac,R. and Ford,J.E.

TITLE Direct Submission

JOURNAL Submitted (13-SEP-1999) Functional Genomics, HYSEQ Inc., 670

FEATURES

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11	42	100.0	7605	6	AR221131	Sequence
12	42	100.0	7605	6	AR302959	Sequence
13	42	100.0	7605	6	AC069311	Sequence
14	42	100.0	197308	9	AC016724	Homo sapi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Nicklin,M. and Barton,J.
The il-11 gene and polypeptide products
Patent: WO 0105974-A 16 25-JAN-2001;
Interleukin Genetics, Inc. (US)

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RESULT 3

HSA242738

LOCUS

HSA242738 2604 bp mRNA linear PRI 18-APR-2002
Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L1 gene)
transcript 2.

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

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	REFERENCE	1 Nicklin,M. and Barton,J. The il-1l1 gene and polypeptide products Patent: WO 0105974-A 43 25-JAN-2001; Interleukin Genetics, Inc. (US)
	AUTHORS	Nicklin,M. and Barton,J.
	TITLE	The il-1l1 gene and polypeptide products
	JOURNAL	Patent: WO 0105974-A 43 25-JAN-2001; Interleukin Genetics, Inc. (US)
	FEATURES	Location/Qualifiers source 1. .6540 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
	ORIGIN	Query Match 100.0%; Score 42; DB 6; Length 6540; Best Local Similarity 100.0%; Pred. No. 0.0012; Mismatches 0; Indels 0; Gaps 0; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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	RESULT 6	HSA271338 LOCUS HSA271338 6540 bp DNA linear PRI 18-APR-2002 DEFINITION Homo sapiens IL1L1 gene for interleukin-1 like protein 1, exons
	ACCESSION	Version 1
	KEYWORDS	Accession HSA271338
	SOURCE	Definition Homo sapiens IL1L1 gene; Interleukin-1 like protein 1. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	REFERENCE	Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
	AUTHORS	Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J.
	TITLE	A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
	JOURNAL	Eur. J. Immunol. 30 (11), 3299-3308 (2000)
	MEDLINE	20545212 PubMed 11093146
	PUBMED	11093146
	REFERENCE	2 (bases 1 to 6540) Nicklin,M.J.H. Direct Submission Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
	AUTHORS	Nicklin,M.J.H.
	TITLE	Direct Submission
	JOURNAL	Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
	FEATURES	Location/Qualifiers source 1. .6540 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="2" /map="2q13" /clone="PAC 131J6" 451. .6522 /gene="IL1L1" Join(<451..524,1193..1248,2631..2716,3905..4032, 4234..6522) /gene="IL1L1" 451. .524 /gene="IL1L1" 457. .507 /number=1 /gene="IL1L1" /note="unnamed protein product; uORF" /codon_start=1 /protein_id="CAB67703.1" /db_xref="GI:6729587" /db_xref="UniProt/TREMBL:Q9NY32" /translation="MAGRKDRGRKEGEGKE" 525. .968 /gene="IL1L1" Join(<969..1022,1193..1248,2631..2716,3905..4032, 4234..6522) /gene="IL1L1" /note="alternative" 369. .1022 /gene="IL1L1" /number=2 1023. .1192 /gene="IL1L1" /number=2 1193. .1248 /gene="IL1L1" /number=3 Join(1220..1248,2631..2716,3905..4032,4234..4458) /gene="IL1L1" /function="putative cytokine or cytokine antagonist" /codon_start=1 /product="interleukin-1 like protein 1" /protein_id="CAB67704.1" /db_xref="GI:6729588" /db_xref="GOA:Q9UBH0" /db_xref="UniProt/Swiss-Protein:Q9UBH0" /translation="MWLSGALCFRMDKSAIKLVLYHNQLLAGLHGAKVIKGEETISV VNRMLDASLPVLIGVGSGQCLSCGVGGPEPTLTLEFVNIMELYLGAKESKSFYFR RDMLGTSPESAAYPGWFLCTVPADQPVRLTQLPENGGWNAPITDFYQQCD"


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ORIGIN
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Query Match      100.0%; Score 42; DB 6; Length 7605;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
LOCUS AX069311 7605 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 8 from Patent WO0102571.
ACCESSION AX069311
VERSION AX069311.1 GI:12579183
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ford,J. and Pace,A.
TITLE A interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: WO 0102571-A 8 11-JAN-2001;
HYSEQ, INC. (US)
FEATURES
source Location/Qualifiers
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       /mol_type="unassigned DNA"
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ORIGIN

Query Match      100.0%; Score 42; DB 6; Length 7605;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAGGAGGGAGAGGGAAGGAGTGAAGGAAGGAGTGAAG 42
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Db 1339 AAGGAAGGAGGGAGAGGGAAGGAGTGAAGGAAGGAGTGAAG 1380
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RESULT 13
AC016724 197308 bp DNA linear PRI 09-JAN-2002
LOCUS AC016724
DEFINITION Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION AC016724
VERSION AC016724.11 GI:14718389
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 197308)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 197308)
AUTHORS Armstrong,J. and Haakenson,W.
TITLE The sequence of Homo sapiens BAC clone RP11-339F22
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 197308)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1999) Genome Sequencing Center, Washington
MO 63108, USA
REFERENCE 4 (bases 1 to 197308)
AUTHORS Waterston,R.H.

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TITLE
JOURNAL
Direct Submission
Submitted (14-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 197308)
Waterston, R.
AUTHORS
JOURNAL
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 14, 2001 this sequence version replaced gi:13431151.

Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu

Summary Statistics

Center project name: H_NH0339F22

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-725J3, the clone sequenced to the right is RP11-97J14. Actual start of this clone is at base position 1 of RP11-339F22; actual end is at base position 197308 of RP11-339F22.

Data from AC084280 and AC024704 was used to finish this clone, AC016724. Polymorphisms have been identified between AC024704 and AC016724.

Sequence derived from pcr from base position 148683 to 149264.

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repeat_region
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JOURNAL Submitted (03-APR-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 162771)

AUTHORS Wilson.R

TITLE Direct Submission

JOURNAL Submitted (30-MAY-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Apr 3, 2003 this sequence version replaced gi:27923720.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.edu
 ----- Summary Statistics -----
 Center project name: H_NHO366H04

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
 This sequence is not the entire insert of the clone. This clone is overlapped by AC108073.

Data from AC133529 was used to finish this clone.

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repeat_region	2004..2097 /rpt_family="Alu"
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repeat_region	2906..3219 /rpt_family="MaLR"
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jan 29, 2003 this sequence version replaced gi:26006685.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0458M01

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES

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 repeat_region 12528..12835 /rpt_family="Alu"
 repeat_region 12836..13031 /rpt_family="ERV1"
 repeat_region 13234..13331 /rpt_family="GA-rich"
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 repeat_region 13835..13971 /rpt_family="Alu"
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 repeat_region 18978..19816 /rpt_family="Li"
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 repeat_region 20482..20526 /rpt_family="(TG)n"
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:56:15 ; Search time 127.576 Seconds
(without alignments)
11636.250 Million cell updates/sec

Title: US-09-617-720A-2

Perfect score: 39
Sequence: 1 ttgaggaaacagcagactccacagctccgcagagaa 39

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	25	64.1	444	6	CB745486	CB745486 AMGNNUC:M
4	24.8	63.6	264	8	AZ401556	AZ401556 IM0158P17
5	24.8	63.6	854	7	CO805958	CO805958 AGENCOURT
6	24	61.5	805	5	BU354596	BU354596 603473139
7	23.8	61.0	381	2	BE93964	BE93964 UI-M-BZ1-
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9	23.6	60.5	523	1	AV604210	AV604210 AV604210
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14	23	59.0	443	8	BZ206975	BZ206975 CH230-425
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16	22.8	58.5	507	1	AU200748	AU200748 AU200748
17	22.8	58.5	563	4	BJ116536	BJ116536 BJI16536
18	22.8	58.5	629	1	AU200217	AU200217 AU200217
19	22.8	58.5	752	5	BU363211	BU363211 603585713
20	22.6	57.9	365	6	CA360753	CA360753 634412 NC
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C 27	22.2	56.9	247	7	W83796	W83796 mf33c03.r1
C 28	22.2	56.9	255	1	AA184891	AA184891 mu48a08.r
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C 30	22.2	56.9	274	1	AA015339	AA015339 mh13b08.r
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C 33	22.2	56.9	356	5	BY467369	BY467369 BY467369
C 34	22.2	56.9	360	4	BG090598	BG090598 mac08f06.
C 35	22.2	56.9	363	2	BB766156	BB766156 BB766156
C 36	22.2	56.9	370	4	BG092249	BG092249 mac07b03.
C 37	22.2	56.9	385	5	BU756272	BU756272 UI-1-CFO-
C 38	22.2	56.9	386	2	BF100852	BF100852 601753788
C 39	22.2	56.9	388	2	BE849929	BE849929 uw09f08.y
C 40	22.2	56.9	391	6	BY527295	BY527295 UI-M-BZ1-
C 41	22.2	56.9	401	2	BE989206	BE989206 UI-M-BZ1-
C 42	22.2	56.9	416	4	BM668586	BM668586 UI-E-CK1-
C 43	22.2	56.9	418	1	AI414767	AI414767 ms59h02.x
C 44	22.2	56.9	442	1	AA267559	AA267559 val6908.r
C 45	22.2	56.9	448	2	BE989363	BE989363 UI-M-BZ1-

ALIGNMENTS

RESULT 1
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DEFINITION DKFZp686022193_5', mRNA sequence.
ACCESSION BX477358
VERSION BX477358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
TITLE EST (Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Heidelberg/Germany) within the CDNA sequencing consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686022193) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1..338
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686022193"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN

Query Match 66.7%; Score 26; DB 5; Length 338;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 14 AGATCCACAGCTCCGCCAGGAGAA 39
|||||
Db 1 AGATCCACAGCTCCGCCAGGAGAA 26

RESULT 2
AW141829/c
LOCUS AW141829.1 424 bp mRNA linear EST 30-OCT-1999
DEFINITION EST291936 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
RGIC187 5' end similar to guanine nucleotide-binding protein Rat,
mRNA sequence.
ACCESSION AW141829
VERSION AW141829.1 GI:6161680
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 424)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
Index (http://www.tigr.org/db/rat/rat/rat.html). To order a clone
contact the ATCC (http://www.atcc.org/atcc.html).
Seq primer: M13 Reverse.
Location/Qualifiers
1..424
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RGIC187"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"

FEATURES
source
1..424
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RGIC187"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"

ORIGIN
Query Match 64.1%; Score 25; DB 2; Length 424;
Best Local Similarity 84.8%; Pred. No. 1.6e+02;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GAACAGCAGACTCCACAGCTCCGCCAGGAGA 38
|||||
Db 343 GAACAGCGGAGACCCACAGCTCCCGTAGGAGA 311

RESULT 3
CB745486/c
LOCUS CB745486.1 444 bp mRNA linear EST 11-APR-2003
DEFINITION AMGNNUC:MRBE3-00043-A6-A rat brain E15 (10374) Rattus norvegicus
cDNA clone mrbe3-00043-a6 5', mRNA sequence.
ACCESSION CB745486
VERSION CB745486.1 GI:29812788
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 444)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program

JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 0043 row: a column: 6.
Location/Qualifiers
1..444
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="mrbe3-00043-a6"
/tissue_type="brain E15"
/clone_lib="rat brain E15 (10374)"
/note="Vector: pBCB; Site_1: BstXI; Site_2: NotI; rat
brain E15"

FEATURES
source
1..444
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="mrbe3-00043-a6"
/tissue_type="brain E15"
/clone_lib="rat brain E15 (10374)"
/note="Vector: pBCB; Site_1: BstXI; Site_2: NotI; rat
brain E15"

ORIGIN
Query Match 64.1%; Score 25; DB 6; Length 444;
Best Local Similarity 84.8%; Pred. No. 1.6e+02;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GAACAGCAGACTCCACAGCTCCGCCAGGAGA 38
|||||
Db 366 GAACAGCGGAGACCCACAGCTCCCGTAGGAGA 334

RESULT 4
AZ401556
LOCUS AZ401556
DEFINITION IM0168P17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0168P17 F, genomic survey sequence.
ACCESSION AZ401556
VERSION AZ401556.1 GI:10516630
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 264)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 17
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 264.
Location/Qualifiers
1..264
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0168P17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```


(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.6%; Score 24.8; DB 8; Length 264;
Best Local Similarity 80.6%; Pred. No. 1.8e+02;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GAGGACAGCAGACTCCACAGCTCCGCCAGGAGA 38
|||||
DB 113 GAGGACAGCAGACTCCACAGCTCCGCCAGGAGA 148
|||||

RESULT 5

C0805958/c

LOCUS

DEFINITION AGENCOURT_30259104 NIH_MGC_256 Mus musculus cDNA clone
IMAGE:30935315 5', mRNA sequence.

ACCESSION

C0805958

VERSION

C0805958.1

KEYWORDS

EST.

SOURCE

MUS MUSCULUS (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAML189 row: d column: 12

High quality sequence stop: 562.

Location/Qualifiers.

1. .854

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:30935315"

/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_256"

/notes="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;

Site 2: NotI; cDNA was primed using oligo-dr primer:

5'-pGACTGTTCTACATCGCAGCGGCCCT(T)25-3' and cloned into

the EcoRV/NotI sites of pExpress-1. Size-selection 0.5 kb

resulted in an average insert size of 1.2 kb. This is a

primary library (normalized primary library is NIH_MGC_257)

and was constructed by Express Genomics (Frederick, MD).

Note: this is a NIH_MGC library"

ORIGIN

Query Match 63.6%; Score 24.8; DB 7; Length 854;
Best Local Similarity 80.6%; Pred. No. 1.9e+02;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GAGGACAGCAGACTCCACAGCTCCGCCAGGAGA 38
|||||
DB 57 GAGGACAGCAGACTCCACAGCTCCGCCAGGAGA 22
|||||

RESULT 6

BU354596/c

LOCUS

DEFINITION

BU354596

VERSION

BU354596.1

KEYWORDS

EST.

SOURCE

GALLUS GALLUS (chicken)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .805

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="ChEST352n10"

/dev_stage="36"

/lab_host="DH10B"

/clone_lib="CSEQCHN70"

/note="Organ: hearts; Vector: pBluescript II KS(+);

Site 1: EcoRI; Site 2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was bluntended, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

ORIGIN

Query Match 61.5%; Score 24; DB 5; Length 805;
Best Local Similarity 84.4%; Pred. No. 3.8e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTGAGNACAGCAGACTCCACAGCTCCCGCC 32
|||||
DB 34 TTGAGNACAGCAGACTCCACAGCTCCGAGCC 3
|||||

```

RESULT 7
BE993964
LOCUS
DEFINITION
  UI-M-BZ1-bj1-b-01-0-UI.s1 NIH BMAP_MHI2_S1 Mus musculus cDNA clone
  UI-M-BZ1-bj1-b-01-0-UI 3', mRNA sequence.
ACCESSION
BE993964
VERSION
BE993964.1
KEYWORDS
  GI:10676702
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 381)
AUTHORS
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
  Normalization and subtraction: two approaches to facilitate gene
  discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
889548
COMMENT
  Contact: Chin, H
  National Institute of Mental Health
  6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
  20892-9643, USA
  Tel: 301 443 1706
  Fax: 301 443 9890
  Email: mES@mail.nih.gov
  The sequence contained an oligo-dT track that was present in the
  oligonucleotide that was used to prime the synthesis of first
  strand cDNA and therefore this may represent a bonafide poly A
  tail. cDNA Library Preparation: M.B. Soares lab Clone distribution:
  Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
  should be noted that Bento Soares is generating a small number of
  additional specialized non-redundant arrays of BMAP cDNAs whose
  availability will be considered under appropriate and limited
  collaborative arrangements the following repetitive elements were
  found in this cDNA sequence: 1-30, >AT-rich#Low_complexity
  Seq primer: M13 Forward
  POLYA=Yes.

FEATURES
  source
  1..381
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UI-M-BZ1-bj1-b-01-0-UI"
  /dev_stage="27-32 days"
  /lab_host="DH10B (Life Technologies)"
  /clone_lib="NIH BMAP_MHI2_S1"
  /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
  polylinker; Site 1: Not 1; Site 2: Eco RI; The
  NIH BMAP_MHI2_S1 library is a subtracted library derived
  from NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived
  from mouse hippocampus tissue. For a detailed description
  of the library from which this clone was derived, please
  visit our web site at brainest.eng.uiowa.edu.
  TAG_SEQ=None found"

ORIGIN
Query Match 61.0%; Score 23.8; DB 2; Length 381;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TGAGGACAGGCAGACTCCACAGCTCCGCCAGGA 36
  ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 TGACCAGGAGGCAGACTCCACTGCTCTGACAGGA 209

RESULT 8
CK931100/c
LOCUS
DEFINITION
  CK931100
  4054658 BARC 8BOV Bos taurus cDNA clone 8BOV_22G04 5', mRNA
  sequence.

FEATURES
  source
  1..633
  /organism="Bos taurus"
  /mol_type="mRNA"
  /strain="Holstein"
  /db_xref="taxon:9913"
  /clone="8BOV_22G04"
  /sex="Female"
  /tissue_type="Epithelial, Muscle"
  /dev_stage="Lactating, Neonatal"
  /lab_host="DH10B TonA"
  /clone_lib="BARC 8BOV"
  /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
  Not1; Site 2: EcoRI; Normalized cow cDNA intestinal_
  library in pCMVSPORT6.1, constructed from equimolar mRNA
  pools derived from 5 sources, 4 lactating from equimolar mRNA
  neonatal intestinal 4/5 Lactating, Proximal Duodenum,
  Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
  Duodenum, Jejunum, Distal Ileum"

ORIGIN
Query Match 61.0%; Score 23.8; DB 7; Length 633;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTGAGAACAGGCAGACTCCACAGCTCCGCCAGG 35
  ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 455 TTGAGAACATCTCGCTCCAGAGCTCCCTGCAGG 421

RESULT 9
AV604210
LOCUS
DEFINITION
  AV604210 Bos taurus kidney fetus Bos taurus cDNA clone EIKI021D06
  3', mRNA sequence.
ACCESSION
AV604210
VERSION
AV604210.1
KEYWORDS
  GI:9734583
SOURCE
  EST.
ORGANISM
  Bos taurus (cow)
  Bos taurus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovinae; Bos.
  1 (bases 1 to 523)
AUTHORS
  Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
  and Sugimoto,Y.

```

TITLE Establishment of a high throughput EST sequencing system using Poly(A) tail-removed cDNA libraries and determination of 36,000 Bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)

MEDLINE 21570554

PUBMED 11713328

COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cococ.ocn.ne.jp

Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

source

1. .523
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="EIKI021D06"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
/clone_lib="Bos taurus kidney fetus"
/note="Vector: pZLI; Site_1: SalI; Site_2: NotI; Poly A was deleted from a NotI site"

ORIGIN

Query Match 60.5%; Score 23.6; DB 1; Length 523;
Best Local Similarity 76.3%; Pred. No. 5.2e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGAGGAACAGGAGACTCCACAGCTCCGCCAGGAGAA 39
|||||
Db 466 TCAGGATCGACAGACTCCAGTCTCCAGCCAGCA 503

RESULT 10

BX373721

LOCUS BX373721 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1071YH11 3-PRIME, mRNA sequence.
DEFINITION BX373721 EST.

BX373721

BX373721.1 GI:30438340

EST.

Homo sapiens (human)

Homo sapiens

SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1046)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

JOURNAL**TITLE****COMMENT**

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1718.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0BAK063CB10NMI&c=1718.f>.

FEATURES

source

1. .1046
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1071YH11"
/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 60.5%; Score 23.6; DB 5; Length 1046;
Best Local Similarity 76.3%; Pred. No. 5.3e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGAGGAACAGGAGACTCCACAGCTCCGCCAGGAGAA 39
|||||
Db 576 TCAGGACAGGAGACTCACTGCTCTCCAGTAGAA 613

RESULT 11

CE232012

LOCUS

DEFINITION tigr-gss-dog-1700033348863 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION CE232012

VERSION

CE232012.1 GI:35387770

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE**AUTHORS**

1 (bases 1 to 656)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

MEDLINE

PUBMED

COMMENT

Contact: Kirkness EF

The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

FEATURES

source

1. .656
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 59.5%; Score 23.2; DB 9; Length 656;
Best Local Similarity 77.8%; Pred. No. 7.3e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 AGAAGAGGAGACTCCACAGCTCCGCCAGGAGAA 39
|||||
Db 503 AGAAGATCGAGTAGACAGATCCAGCCAGGTGA 538

RESULT 12

BP700567

LOCUS

DEFINITION BP700567 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library Xenopus laevis cDNA clone XL490c06ex 5', mRNA sequence.
ACCESSION BP700567

VERSION

BP700567.1 GI:46048839

KEYWORDS

SOURCE

Xenopus laevis (African clawed frog)

```

ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE
1 (bases 1 to 766)

AUTHORS
Osada,S., Kitayama,A., Ueno,N. and Taira,M.

TITLE
Expression analysis of genes which are expressed in the anterior
neuroectoderm of Xenopus embryos

JOURNAL
Unpublished (2004)

COMMENT
Contact: Masanori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m_taira@biol.s.u-tokyo.ac.jp,
URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.

FEATURES
source
1..766
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL490C06ex"
/tissue_type="anterior neuroectoderm"
/dev_stage="late gastrula (stage 12.5)"
/clone_lib="Osada Taira anterior neuroectoderm (ANE)
PCS105 cDNA library"

ORIGIN
Query Match 59.5%; Score 23.2; DB 5; Length 766;
Best Local Similarity 77.8%; Pred. No. 7.4e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 AGGAACAGGAGGAGTCCACAGCTCCGCCAGGAGAA 39
|||||
Db 439 AGGAACAGGAGGAGTCCACAGCTCCATCAGAGGAA 474
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RESULT 13
BU708233 794 bp mRNA linear EST 15-JUL-2003
LOCUS
UI-M-FCO-caq-b-10-0-UI.r1 NIH_BMAP_FCO Mus musculus cDNA clone
IMAGE:6415785 5', mRNA sequence.

REFERENCE
BU708233 1 GI:23640494
EST.
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 794)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..794
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="C57BL/6"
/db_xref="taxon:10090"

FEATURES
source
1..794
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCw"
/db_xref="taxon:10116"

/clone="IMAGE:6415785"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_FCO"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is TGAGAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match 59.5%; Score 23.2; DB 5; Length 794;
Best Local Similarity 75.7%; Pred. No. 7.4e+02;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGAGAAACAGGAGGAGTCCACAGCTCCGCCAGGAGAA 38
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Db 695 TGAGAAAGAGGACACTCTCTGCGCCGCTGGAGA 731
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RESULT 14
BU708233 443 bp DNA linear GSS 11-OCT-2002
LOCUS
CH230-42508.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
IMAGE:6415785 5', genomic survey sequence.

REFERENCE
BU708233 1 GI:23865027
GSS.
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 443)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-42508.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_end/rat/bac_end_intro.html
Plate: 425 row: 0 column: 8
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..443
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCw"
/db_xref="taxon:10116"

FEATURES
source
1..443
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCw"
/db_xref="taxon:10116"

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/clone="CH230-42508"

/sex="Female"

/cell_type="Brain"

/clone_lib="CHORI-230 Segment 2"

/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;

CHORI-230 Rat (BN/NaNHd/MCW) BAC library produced by

Pieter de Jong"

ORIGIN

Query Match 59.0%; Score 23; DB 8; Length 443;

Best Local Similarity 74.4%; Pred. No. 8.4e+02;

Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TTGAGGACAGGAGACTCCACAGCTCCGCCAGGAGAA 39

| | | | | | | | | | | | | | | | | | | | |

Db 22 TAGAGGACAGGAGAAACCCAAAGCCCGCAGTCAGGGAA 60

RESULT 15

AI762761/c

LOCUS

DEFINITION wh83e11.x1 NCI_CGAP_CLL1 Homo sapiens CDNA clone IMAGE:2387372 3',

mRNA sequence.

AI762761

AI762761.1 GI:5178428

EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1107 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 477.

Location/Qualifiers

FEATURES

source

1..490

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2387372"

/tissue_type="B-cell, chronic lymphocytic leukemia"

/lab_host="DH10B"

/clone_lib="NCI CGAP CLL1"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand CDNA

was primed with a Not I - oligo(dT) primer [5,

T 3']; double-stranded CDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 58.5%; Score 22.8; DB 1; Length 490;

Best Local Similarity 79.4%; Pred. No. 1e+03;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GAGGAACAGGACAGACTCCACAGCTCCCGCAGGA 36

Db 278 GAGCAACAGGGAATTCACAGCTGCTCCAGAA 245

Search completed: March 13, 2005, 18:13:56

Job time : 142.576 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:14:57 ; Search time 172.432 Seconds
(without alignments)
10959.418 Million cell updates/sec

Title: US-09-617-720A-2
Perfect score: 39
Sequence: 1 ttgaggaaacaggcagactccacagctccgcccaggagaa 39

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	6	AX080390 Sequence
2	39	100.0	2613	9	AJ242737 Homo sapi
3	37.4	95.9	54	6	AX080406 Sequence
4	37.4	95.9	2701	6	CQ722801 Sequence
5	37.4	95.9	2720	9	AF186094 Sequence
6	37.4	95.9	5751	6	BD211436 A novel i
7	37.4	95.9	5751	6	AR181996 Sequence
8	37.4	95.9	5751	6	AR221130 Sequence
9	37.4	95.9	5751	6	AR302958 Sequence
10	37.4	95.9	5751	6	AX069310 Sequence
11	37.4	95.9	6540	9	AX080431 Sequence
12	37.4	95.9	6540	9	AJ271338 Homo sapi
13	37.4	95.9	7604	9	AF216693 Homo sapi
14	37.4	95.9	7605	6	BD211437 A novel i
15	37.4	95.9	7605	6	AR181997 Sequence
16	37.4	95.9	7605	6	AR221131 Sequence
17	37.4	95.9	7605	6	AR302959 Sequence
18	37.4	95.9	7605	6	AX069311 Sequence
19	37.4	95.9	197308	9	AC016724 Homo sapi

C	20	29.4	75.4	197308	9	AC016724	Homo sapi
C	21	25.4	65.1	90147	2	AC135832	Rattus no
C	22	25	64.1	247903	2	AC127185	Rattus no
C	23	24.8	63.6	7733	10	AF233337	Mus muscu
C	24	24.8	63.6	91841	10	AL606971	Mouse DNA
C	25	24.4	62.6	125495	9	AL359914	Human DNA
C	26	23.8	61.0	154708	2	AC024443	Homo sapi
C	27	23.8	61.0	170979	9	AC007950	Homo sapi
C	28	23.8	61.0	171456	9	AC023591	Homo sapi
C	29	23.8	61.0	177432	9	AC118274	Homo sapi
C	30	23.8	61.0	203912	9	AC008755	Homo sapi
C	31	23.8	61.0	230882	9	AC131689	Mus muscu
C	32	23.2	59.5	3868	5	BC073106	Xenopus l
C	33	23.2	59.5	149556	9	AC146478	Pan trogl
C	34	23.2	59.5	198155	2	BS000632	Human DNA
C	35	23	59.0	101196	9	HS463A9	Human DNA
C	36	23	59.0	214497	2	AC102558	Mus muscu
C	37	23	59.0	279315	2	AC132765	Rattus no
C	38	23	59.0	342581	2	AC132742	Rattus no
C	39	22.8	58.5	3071	6	CQ609104	Sequence
C	40	22.8	58.5	31261	3	U41278	Caenorhabdi
C	41	22.8	58.5	45258	2	AC015395	Drosophil
C	42	22.8	58.5	144090	2	AC150031	Dasyopus n
C	43	22.8	58.5	175223	9	AC004617	Homo sapi
C	44	22.8	58.5	186218	3	AC023680	Drosophil
C	45	22.8	58.5	245482	2	AC110679	Rattus no

ALIGNMENTS

RESULT 1
AX080390
LOCUS AX080390 39 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 2 from Patent WO0105974.
ACCESSION AX080390
VERSION AX080390.1 GI:13159841
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nicklin,M. and Barton,J.
TITLE The il-11 gene and polypeptide products
JOURNAL Patent: WO 0105974-A 2 25-JAN-2001,
Interleukin Genetics, Inc. (US)
FEATURES
source
1..39
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 39; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAGAAACAGGAGACTCCACAGCTCCGCCAGGAGAA 39
DB 1 TTGAGAAACAGGAGACTCCACAGCTCCGCCAGGAGAA 39
RESULT 2
HSA242737 2613 bp mRNA linear PRI 18-APR-2002
LOCUS HSA242737
DEFINITION Homo sapiens mRNA for interleukin-1-like protein-1 (IL1L1 gene),
transcript 1.
ACCESSION AJ242737
VERSION AJ242737.1 GI:6165333
KEYWORDS IL1L1 gene; interleukin-1-like protein-1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Barton,J.L., Herbst,R., Bosio,D., Higgins,L. and Nicklin,M.J.
A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
Eur. J. Immunol. 30 (11), 3299-3308 (2000)
20545212
11093146
2 (bases 1 to 2613)
Nicklin,M.J.
Direct Submission
Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Glossop Road, Sheffield, S10 2UF, UNITED KINGDOM
Location/Qualifiers
1. .2613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosomes="2"
/map="2q12-13"
/tissue_type="placenta"
/notes="Between IL1B and IL1RN"
/genes="IL1L1"
1. .2613
82. 549
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/product="interleukin-1-like protein-1"
/protein_id="CAB59822.1"
/db_xref="GI:6165334"
/db_xref="GOA:Q9UBH0"
/db_xref="UniProt/Swiss-Prot:Q9UBH0"
/translation="WVLSGALCFRMDKSAKLYLHNNQLLAGLHAGKVIKGEISV
VFNRLDASLSPVILGVQSGQCLSGVGQEPFLTLEPVNIMELYLGAKESKSPFYR
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2613
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/citation=[1]
/evidence=experimental

polya_site
2613

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Query Match 100.0%; Score 39; DB 9; Length 2613;
Best Local Similarity 100.0%; Pred. No. 0.0026; Mismatches 0; Indels 0; Gaps 0;
Matches 39; Conservative 0

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Db 1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 39
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RESULT 3
AX080406
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX080406 54 bp DNA linear PAT 22-FEB-2001
Sequence 18 from Patent WO0105974.
AX080406
AX080406.1 GI:13159848
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Nicklin,M. and Barton,J.
The il-1l1 gene and polypeptide products
Patent: WO 0105974-A 18 25-JAN-2001;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
1. .54
/organism="Homo sapiens"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 97.4%; Pred. No. 0.0022; Mismatches 1; Indels 0; Gaps 0;
Matches 38; Conservative 0

QY 1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 39
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2 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 40

Db 2 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 40
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RESULT 4
CQ722801
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CQ722801 2701 bp DNA linear PAT 03-FEB-2004
Sequence 8735 from Patent WO02068579.
CQ722801
CQ722801.1 GI:42283658
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 8735 06-SEP-2002;
PE Corporation
Location/Qualifiers
1. .2701
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN
Query Match 95.9%; Score 37.4; DB 6; Length 2701;
Best Local Similarity 97.4%; Pred. No. 0.0011; Mismatches 1; Indels 0; Gaps 0;
Matches 38; Conservative 0

QY 1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 39
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82 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 120

Db 82 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGAGAA 120
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RESULT 5
AF186094
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF186094 2720 bp mRNA linear PRI 16-OCT-1999
Homo sapiens interleukin-1 receptor antagonist homolog (IL1HV1)
mRNA, complete cds.
AF186094
AF186094.1 GI:6049804
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R.,
Drmanac,R. and Ford,J.E.
IL1HV1: A novel interleukin-1 receptor antagonist gene
Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)
99443727
10512743
2 (bases 1 to 2720)
Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R.,
Drmanac,R. and Ford,J.E.
Direct Submission
Submitted (13-SEP-1999) Functional Genomics, HVSEQ Inc., 670
Almanor Ave., Sunnyvale, CA 94086, USA
Location/Qualifiers
1. .2720

Db 813 TGGAGGAACAGGCAGAGACTCCACAGTCCCGCCAGGAGAA 851

RESULT 7
 AR181996
 LOCUS AR181996 5751 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 7 from patent US 6337072.
 ACCESSION AR181996
 VERSION AR181996.1 GI:20224912
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5751)
 AUTHORS Ford,J. and Pace,A.
 TITLE Interleukin-1 receptor antagonist and recombinant production thereof
 JOURNAL Patent: US 6337072-A 7 08-JAN-2002;
 FEATURES
 source Location/Qualifiers
 source 1..5751
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 95.9%; Score 37.4; DB 6; Length 5751;
 Best Local Similarity 97.4%; Pred. No. 0.00092;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGAACAGGCAGAGACTCCACAGTCCCGCCAGGAGAA 39
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 Db 813 TGGAGGAACAGGCAGAGACTCCACAGTCCCGCCAGGAGAA 851

RESULT 8
 AR221130
 LOCUS AR221130 5751 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 7 from patent US 6426191.
 ACCESSION AR221130
 VERSION AR221130.1 GI:23328015
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5751)
 AUTHORS Ford,J. and Pace,A.
 TITLE Assays involving an IL-1 receptor antagonist
 JOURNAL Patent: US 6426191-A 7 30-JUL-2002;
 FEATURES
 source Location/Qualifiers
 source 1..5751
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 95.9%; Score 37.4; DB 6; Length 5751;
 Best Local Similarity 97.4%; Pred. No. 0.00092;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGAACAGGCAGAGACTCCACAGTCCCGCCAGGAGAA 39
 ||||||||||||||||||||||||||||||||||||||||
 Db 813 TGGAGGAACAGGCAGAGACTCCACAGTCCCGCCAGGAGAA 851

RESULT 9
 AR302958
 LOCUS AR302958 5751 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 7 from patent US 6541623.
 ACCESSION AR302958
 VERSION AR302958.1 GI:31691558
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5751)

AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.
TITLE Interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: US 6541623-A 7 01-APR-2003,
FEATURES Location/Qualifiers
source 1..5751
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 95.9%; Score 37.4; DB 6; Length 5751;
Best Local Similarity 97.4%; Pred. No. 0.00092;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
Db 813 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 851

RESULT 10

AX069310 5751 bp DNA linear PAT 25-JAN-2001

LOCUS Sequence 7 from Patent WO0102571.

ACCESSION AX069310

VERSION AX069310.1 GI:12579182

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Ford, J. and Pace, A.

A interleukin-1 receptor antagonist and uses thereof

PATENT: WO 0102571-A 7 11-JAN-2001;

HYSEQ, INC. (US)

FEATURES Location/Qualifiers

source 1..5751

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Db 813 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 851

RESULT 11

AX080431 6540 bp DNA linear PAT 22-FEB-2001

LOCUS Sequence 43 from Patent WO0105974.

ACCESSION AX080431

VERSION AX080431.1 GI:13159871

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Nicklin, M. and Barton, J.

The il-11 gene and polypeptide products

PATENT: WO 0105974-A 43 25-JAN-2001;

Interleukin Genetics, Inc. (US)

FEATURES Location/Qualifiers

source 1..6540

/organism="Homo sapiens"

/mol_type="unassigned DNA"

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Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 970 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 1008

RESULT 12

HS271338 6540 bp DNA linear PRI 18-APR-2002

LOCUS Homo sapiens IL11 gene for interleukin-1 like protein 1, exons

DEFINITION 1-6.

ACCESSION AJ271338

VERSION AJ271338.1 GI:6729586

KEYWORDS IL11 gene; interleukin-1 like protein 1.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Barton, J.L., Herbst, R., Bosio, D., Higgins, L. and Nicklin, M.J.

A tissue specific IL-1 receptor antagonist homolog from the IL-1

cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities

Eur. J. Immunol. 30 (11), 3299-3308 (2000)

MEDLINE 20545212

PUBMED 11093146

REFERENCE 2 (bases 1 to 6540)

AUTHORS Nicklin, M.J.H.

Direct Submission

Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and

Genetic Medicine, University of Sheffield, Royal Hallamshire

Hospital, Sheffield, South Yorkshire, UNITED KINGDOM

FEATURES Location/Qualifiers

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Best Local Similarity 97.4%; Pred. No. 0.0009;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13
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LOCUS
DEFINITION Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1)
gene, complete cds.
ACCESSION AF216693
VERSION AF216693.1 GI:8572054
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 7604)
AUTHORS Mulero,J.J., Nelken,S.T. and Ford,J.E.
TITLE Organization of the human interleukin-1 receptor antagonist gene
IL1HY1
JOURNAL Immunogenetics 51 (6), 425-428 (2000)
MEDLINE 20322477
PUBMED 10866108
REFERENCE
2 (bases 1 to 7604)
AUTHORS Mulero,J.J., Nelken,S.T. and Ford,J.E.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1999) Functional Genomics, HYSEQ Inc, 670 Almanor
Ave., Sunnyvale, CA 94086, USA
FEATURES
Location/Qualifiers
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Best Local Similarity 97.4%; Pred. No. 0.00087;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14
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LOCUS
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211437
VERSION BD211437.1 GI:33021207
KEYWORDS JP 2002510492-A/6.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 7605)
AUTHORS Ford,J. and Pace,A.
TITLE A novel interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: JP 2002510492-A 6 09-APR-2002;
HYSEQ INC
COMMENT
OS Homo sapiens (human)
PN JP 2002510492-A/6
PD 09-APR-2002
PF 05-APR-1999 JP 2000542457
PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
17-FEB-1999 US 09/251370
PI JOHN FORD, ANN PACE
PC C12N15/09,A61K39/00,C07K14/52,C07K16/24,C12N1/15,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
C12N15/00,
PC A61K37/02,C12N5/00
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2514.2	98.1	2598	6 ABL88229	AbL88229 Human PRO
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35	2514.2	98.1	2598	10 ADC52479	AdC52479 Novel hum
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ALIGNMENTS

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AC AAF27921;
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DT 08-MAY-2001 (first entry)
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DE Human IL-IL1 coding sequence.
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KW Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
KW osteoporosis; systemic lupus erythematosus; ss.
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OS Homo sapiens.
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FT /note= "this region is specifically claimed"

XX WO200105974-A2.
XX
XX 25-JAN-2001.
XX
XX 17-JUL-2000; 2000WO-US019508.
XX
XX 16-JUL-1999; 99US-0144298P.
XX
XX (INTE-) INTERLEUKIN GENETICS INC.
XX
XX PI Nicklin M, Barton J;
XX
XX WPI; 2001-091974/10.
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XX Nucleic acids encoding human and murine interleukin-IL1 polypeptides
XX useful for controlling inflammatory processes.
XX
XX Claim 12; Fig 1; 150pp; English.
XX
XX The present invention provides the protein and coding sequences of the


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QY 1981 CAGAAGCTTGGAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTAGAGGGATAACGGCT 2040
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XX DT 15-MAY-2001 (first entry)
XX DE Human PRO4342 cDNA.
XX KW Human; PRO protein; mapping; ss.
XX OS Homo sapiens.
XX PN WO200116318-A2.
XX PD 08-MAR-2001.
XX PF 24-AUG-2000; 2000WO-US023328.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 07-DEC-1999; 99US-0169495P.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 11-JAN-2000; 2000US-0175481P.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 03-MAR-2000; 2000US-0187202P.
XX PR 21-MAR-2000; 2000US-0191007P.
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PR 10-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX (GETH ) GENENTECH INC.
XX PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX DR P-PSDB; AAB87601.
XX WPI; 2001-183260/18.
XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX PT biology, including use as hybridization probes, and in chromosome and
XX PT gene mapping.
XX PS Claim 2; Fig 151; 278pp; English.
XX CC The present sequence is the coding sequence for a human PRO polypeptide
XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
XX CC antagonists or anti-PRO antibodies are useful for preparation of a
XX CC medicament useful in the treatment of a condition which is responsive to
XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
XX CC protein may also be employed as molecular weight markers for protein
XX CC electrophoresis. The PRO coding sequence has applications in molecular
XX CC biology, including use as hybridisation probes, and in chromosome and
XX CC gene mapping
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
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QY 481 TCCAGCAGTGTGACTAGGGCAACGTCGCCCCCCAGAACTCCTCTGGGACAGCCAGCTCGG 540
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Qy 1080 AGCTCAGAGATAAAGATAAGTAGGATGCTGATGCTCAGAGAAATGGTTCCG 1139
Db 1117 AGCTCAGAGATAAAGATAAGTAGGATGCTGATGCTCAGAGAAATGGTTCCG 1176
Qy 1140 ATCAAAATCCAGATGCTGCTCTATTCCCATGAAAGAGTGTCAATGATATTCAGAA 1199
Db 1177 ATCAAAATCCAGATGCTGCTCTATTCCCATGAAAGAGTGTCAATGATATTCAGAA 1236
Qy 1200 GACCTACTTCAAAAGTGGCATAATATGCAATTTATTTAATTAAGATACCTATTATA 1259
Db 1237 GACCTACTTCAAAAGTGGCATAATATGCAATTTATTTAATTAAGATACCTATTATA 1296
Qy 1260 TATTTCTTTATAGAAAAGTCTGGAAGAGTTTACTTCAATTCAGCAATGTCAGGGTGG 1319
Db 1297 TATTTCTTTATAGAAAAGTCTGGAAGAGTTTACTTCAATTTGAGCAATGTCAGGGTGG 1356
Qy 1320 TGGCAGTATAGGTGATTTTCTTTTAAATCTGTGTAATTTATCTGTATTTCTTAATTTTC 1379
Db 1357 TGGCAGTATAGGTGATTTTCTTTTAAATCTGTGTAATTTATCTGTATTTCTTAATTTTC 1416
Qy 1380 TACAATGAAGATGAATTTCTTGTAATAAATAAGAAAAGAAATTAATCTTTGAGGTAGCA 1439
Db 1417 TACAATGAAGATGAATTTCTTGTAATAAATAAGAAAAGAAATTAATCTTTGAGGTAGCA 1476
Qy 1440 GAGCAGACATCATCTCTGATGTCCTCAGCTCCAATTTCCCGAGATTAATTCATAATGA 1499
Db 1477 GAGCAGACATCATCTCTGATGTCCTCAGCTCCAATTTCCCGAGATTAATTCATAATGA 1536
Qy 1500 ATCCAGTCTGCTCTCTGTTGGTGTGTAGTAGTATGATCAGGAAACAGATCTCAGCAAGC 1559
Db 1537 ATCCAGTCTGCTCTCTGTTGGTGTGTAGTAGTATGATCAGGAAACAGATCTCAGCAAGC 1596
Qy 1560 CACTGAGGAGAGGCTGTGCTGAGATTTGTGGCTGGAATCTCTGGGTAAAGAACTTAAA 1619
Db 1597 CACTGAGGAGAGGCTGTGCTGAGATTTGTGGCTGGAATCTCTGGGTAAAGAACTTAAA 1656
Qy 1620 GAAACAAAATCATCTGGTAATTTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGC 1679
Db 1657 GAAACAAAATCATCTGGTAATTTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGC 1716
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Qy 1680 ATTGATCCAGTCTCTAAGAGGCTGTGTACTGTGTTGAAATTTGTGTCCTCCCTCAAATCA 1739
Db 1717 ATTGATCCAGTCTCTAAGAGGCTGTGTACTGTGTTGAAATTTGTGTCCTCCCTCAAATCA 1776
Qy 1740 CATCTCTTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGCAGATGAG 1799
Db 1777 CATCTCTTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGCAGATGAG 1836
Qy 1800 TTAGTTAAGACAGAGTCTATGCTGAAGTAGACCTAAATTCATATATGACTGTTTCC 1859
Db 1837 TTAGTTAAGACAGAGTCTATGCTGAAGTAGACCTAAATTCATATATGACTGTTTCC 1896
Qy 1860 TTGTATGAAAAGGAGAGACACAGAGACAGAGAGAGACGCGGGAGAGACTATGTAAGATG 1919
Db 1897 TTGTATGAAAAGGAGAGACACAGAGACAGAGAGAGACGCGGGAGAGACTATGTAAGATG 1956
Qy 1920 AAGGACAGATCGAGTTTTCAGCCACACAGCTAAGAAACACCAAGGATTCGCGCAACA 1979
Db 1957 AAGGACAGATCGAGTTTTCAGCCACACAGCTAAGAAACACCAAGGATTCGCGCAACA 2016
Qy 1980 TCAGAGCTTTGGAAGAGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATAACGCG 2039
Db 2017 TCAGAGCTTTGGAAGAGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATAACGCG 2076
Qy 2040 TCTGCTGAAACCTTAATCTCAGACTTCAGCTCTGAAACGAAAGAAATAAATTTCCG 2099
Db 2077 TCTGCTGAAACCTTAATCTCAGACTTCAGCTCTGAAACGAAAGAAATAAATTTCCG 2136
Qy 2100 CTGTTTAAAGCCACCAAGGATAATTTGTTACAGAGCTCTAGGAACTTAATACAGCTGCT 2159
Db 2137 CTGTTTAAAGCCACCAAGGATAATTTGTTACAGAGCTCTAGGAACTTAATACAGCTGCT 2196
Qy 2160 AAAATGATCCCTGCTCTCTCGTGTGTTTACATTTCTGTGTGTCCTCCACAAATGACCA 2219
Db 2197 AAAATGATCCCTGCTCTCTCGTGTGTTTACATTTCTGTGTGTCCTCCACAAATGACCA 2256
Qy 2220 AAGTTGTCTTTGTGACCCAAATAGAAATATGGCAAGATGATGGCATGCCACTTCCAGAT 2279
Db 2257 AAGTTGTCTTTGTGAC-CCAATAGAAATATGGCAAGATGATGGCATGCCACTTCCAGAT 2315
Qy 2280 AGTTTATAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTGCGCAACCCACCCGCC 2339
Db 2316 AGTTTATAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTGCGCAACCCACCCGCC 2375
Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGTGTGTCATGTCATGAGCAGGCTTA 2399
Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGTGTGTCATGTCATGAGCAGGCTTA 2435
Qy 2400 TAAAGAGACTTACGTGGTAAATAAATGAAGTCTCCTGCCACAGCCACACATTAGTGACCTA 2459
Db 2436 TAAAGAGACTTACGTGGTAAATAAATGAAGTCTCCTGCCACAGCCACACATTAGTGACCTA 2495
Qy 2460 GAAGCAGACACTGTGAGATAATCGATGTTTGTGTTTAAAGTGTGCTCAGTTTTGGTCT 2519
Db 2496 GAAGCAGACACTGTGAGATAATCGATGTTTGTGTTTAAAGTGTGCTCAGTTTTGGTCT 2555
Qy 2520 AACTTGTGTTATGAGCAATAGATAAATAATATCCAGAGAAAGAG 2562
Db 2556 AACTTGTGTTATGAGCAATAGATAAATAATATCCAGAGAAAGAG 2598
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RESULT 3

AB574453
ID AB574453 standard; cDNA; 2598 BP.

XX AB574453;

AC (first entry)

XX 10-DEC-2002

XX Human cDNA encoding secreted/transmembrane protein PRO4342.

XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;
 XX articular cartilage defect; osteoarthritis; rheumatoid arthritis.

OS Homo sapiens.

XX US2002119130-A1.

XX 29-AUG-2002.

XX 06-DEC-2001; 2001US-00008667.

XX 29-OCT-1997; 97US-0063435P.

XX 29-OCT-1997; 97US-0064215P.

XX 22-APR-1998; 98US-0082797P.

XX 29-APR-1998; 98US-0083495P.

XX 15-MAY-1998; 98US-0085799P.

XX 02-JUN-1998; 98US-0087759P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088029P.

XX 04-JUN-1998; 98US-0088030P.

XX 10-JUN-1998; 98US-0088734P.

XX 10-JUN-1998; 98US-0088740P.

XX 10-JUN-1998; 98US-0088811P.

XX 10-JUN-1998; 98US-0088824P.

XX 10-JUN-1998; 98US-0088825P.

XX 11-JUN-1998; 98US-0088863P.

XX 12-JUN-1998; 98US-0089105P.

XX 16-JUN-1998; 98US-0089514P.

XX 17-JUN-1998; 98US-0089553P.

XX 19-JUN-1998; 98US-0089952P.

XX 22-JUN-1998; 98US-0090246P.

XX 24-JUN-1998; 98US-0090444P.

XX 25-JUN-1998; 98US-0090688P.

XX 25-JUN-1998; 98US-0090696P.

XX 26-JUN-1998; 98US-0090862P.

XX 02-JUL-1998; 98US-0091828P.

XX 10-AUG-1998; 98US-00956012P.

XX 17-AUG-1998; 98US-0096757P.

XX 18-AUG-1998; 98US-0096949P.

XX 18-AUG-1998; 98US-0096959P.

XX 26-AUG-1998; 98US-0097954P.

XX 26-AUG-1998; 98US-0097971P.

XX 26-AUG-1998; 98US-0097979P.

XX 01-SEP-1998; 98US-0098749P.

XX 10-SEP-1998; 98US-0099741P.

XX 10-SEP-1998; 98US-0099763P.

XX 10-SEP-1998; 98US-0099792P.

XX 10-SEP-1998; 98US-0099812P.

XX 10-SEP-1998; 98US-0099815P.

XX 16-SEP-1998; 98US-0100627P.

XX 16-SEP-1998; 98US-0100662P.

XX 17-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98US-0100683P.

XX 17-SEP-1998; 98US-0100684P.

XX 17-SEP-1998; 98US-0100930P.

XX 22-SEP-1998; 98US-0101279P.

XX 23-SEP-1998; 98US-0101475P.

XX 24-SEP-1998; 98US-0101738P.

XX 24-SEP-1998; 98US-0101743P.

XX 24-SEP-1998; 98US-0101916P.

XX 30-SEP-1998; 98US-0102570P.

XX 06-OCT-1998; 98US-0103449P.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99WO-US010733.

XX 02-JUN-1999; 99WO-US012252.

XX 01-SEP-1999; 99WO-US020111.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021194.

XX 22-DEC-1999; 99WO-US030720.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 01-MAR-2000; 2000WO-US005601.

PR 30-MAR-2000; 2000WO-US008439.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032378.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

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PR 30-MAR-2000; 2000WO-US008439.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032378.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

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30-MAR-2000; 2000WO-US008439.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032378.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 (GETH) GENENTECH INC.
 Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 WPI; 2002-731348/79.
 P-PSDB; ABG95926.
 New isolated secreted and transmembrane PRO polypeptide useful for
 modulating biological activity of a cell, or for treating sports-related
 joint problems, osteoarthritis or rheumatoid arthritis.
 Claim 2; Fig 151; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
 polypeptide having 80 % sequence identity to a sequence appearing as
 ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 extracellular domain of the proteins with their associated signal peptide
 or lacking its associated signal peptide. Also included are the nucleic
 acids encoding the proteins, vectors, host cells, fusion proteins and
 antibodies which specifically bind to the proteins. The proteins are
 useful for detecting a polypeptide designated as A, B, C or D in a sample
 suspected of containing an A, B, C or D polypeptide, by contacting the
 sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 and determining the formation of a A/E, B/F, C/G, C/H or D/I polypeptide
 conjugate in the sample, where the formation of the conjugate is
 indicative of the presence of an A, B, C or D polypeptide in the sample,
 where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 H or I polypeptide is labeled with a detectable label or is attached to a
 solid support. The proteins are useful for linking a bioactive molecule
 to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 or I, or antibodies against them are useful for modulating a biological
 activity of a cell expressing a polypeptide designated as A, B, C or D or
 E, F, G, H, or I. The cell is killed. The proteins are useful for
 identifying agonists or antagonists, for the preparation of a medicament
 useful in the treatment of a condition which is responsive to the
 proteins, as molecular weight markers for protein electrophoresis
 purposes, and as therapeutic agents for treating sports-related joint
 problems, articular cartilage defects, osteoarthritis or rheumatoid
 arthritis. Nucleic acids encoding the proteins are useful as
 hybridisation probes, in chromosome and gene mapping, in the generation
 of anti-sense RNA and DNA, for the preparation of the proteins, to
 generate transgenic or knockout animals which are useful in the
 development and screening of therapeutic useful reagents, for chromosome
 identification, and in gene therapy. The antibody is useful as a
 therapeutic agent, in a diagnostic assay and for affinity purification of
 the protein from recombinant cell culture natural sources. The present
 sequence encodes a novel secreted or transmembrane protein of the
 invention

Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match 98.1%; Score 2514.2; DB 6; Length 2598; Best Local Similarity 99.6%; Pred. No. 0; Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;									
QY	1	AGGGAGCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGCGCTGTGCTTCGAA	60						
DB	38	AGGGAGCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGCGCTGTGCTTCGAA	97						
QY	61	TGAAGGACTCGGCATTGAAGTGCTTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGC	120						
DB	98	TGAAGGACTCGGCATTGAAGTGCTTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGC	157						
QY	121	TGCATCGAGGAAGGCTATTAAAGGTGAAGAGATCAGCGTGGTCCCAATTCGGTGGCTGG	180						
DB	158	TGCATCGAGGAAGGCTATTAAAGGTGAAGAGATCAGCGTGGTCCCAATTCGGTGGCTGG	217						
QY	181	ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGGTGAAGCCAGTGCCTGTCAATGTG	240						
DB	218	ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGGTGAAGCCAGTGCCTGTCAATGTG	277						
QY	241	GGGTGGGAGGAGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	300						
DB	278	GGGTGGGAGGAGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	337						
QY	301	GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT	360						
DB	338	GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT	397						
QY	361	TCAGTGGCTGCTACCGGGGTGCTTCTGTGCAAGTGTGCTGAAGCCGATCAGCCTG	420						
DB	398	TCAGTGGCTGCTACCGGGGTGCTTCTGTGCAAGTGTGCTGAAGCCGATCAGCCTG	457						
QY	421	TCAGACTCACCCAGCTTCCGAGAATGGTGGTGGAAATGCCCCATCAGACTTCTACT	480						
DB	458	TCAGACTCACCCAGCTTCCGAGAATGGTGGTGGAAATGCCCCATCAGACTTCTACT	517						
QY	481	TCAGAGTGTGACTAGGGCAACGTCGCCGCCCCAGAACTCCCTGGGAGAGCCAGCTCGG	540						
DB	518	TCAGAGTGTGACTAGGGCAACGTCGCCGCCCCAGAACTCCCTGGGAGAGCCAGCTCGG	576						
QY	541	GTGAGGGGTGAGTGAAGAGAGACCCATGGCGGCAATCACTCTTCTGCTCTCAGGACCCC	600						
DB	577	GTGAGGGGTGAGTGAAGAGAGACCCATGGCGGCAATCACTCTCTGCTCTCAGGACCCC	636						
QY	601	CAGGTCTGACTTGTAGTGGGCACTGACCACTTTGTCTTCTGGTTCCTAGTTTGCATAAAT	660						
DB	637	CAGGTCTGACTTGTAGTGGGCACTGACCACTTTGTCTTCTGGTTCCTAGTTTGGATAAAT	696						
QY	661	CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCCACTGGATGGTCTACTGCTGTGAAC	720						
DB	697	CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCCACTGGATGGTCTACTGCTGTGAAC	756						
QY	721	CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAATAAGATTTCTGTGGGGTGGG	780						
DB	757	CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAATAAGATTTCTGTGGGGTGGG	816						
QY	781	GTGGGGAGTGTGGGAATCATCTTCTGCTTAAATGTTAACTGACAGTGTACCTTGAGCC	840						
DB	817	GTGGGGAGTGTGGGAATCATTTCTTCTGCTTAAATGTTAACTGACAGTGTACCTTGAGCC	876						
QY	841	CCGAGGCCAACCCATCCAGTTGAGCCTTATAGGGTCACTAGCTCTCCACATGAAGTC	900						
DB	877	CCGAGGCCAACCCATCCAGTTGAGCCTTATAGGGTCACTAGCTCTCCACATGAAGTC	936						
QY	901	CTCTCACTCAACCATGTGAGGAGAGGGAGTGGTCAATAGTCAAGGATCTATGGCCCT	960						
DB	937	CTGTCACTCAACCATGTGAGGAGAGGGAGTGGTCAATAGTCAAGGATCTATGGCCCT	996						
QY	961	TGGCCAGGCCCCACCCCTTCCCTT-ATCCTGCACTGTCTATGCTACCTTCTCTATC	1019						
DB	997	TGGCCAGGCCCCACCCCTTCCCTTTAAATCTCTGCCACTGTCTATGCTACCTTCTCTATC	1056						

QY	241	GGTGGGCGAGCGGACTCTAAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	300
Db	278	GGTGGGCGAGGAGCGGACTCTAAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	337
QY	301	GTGCCAAGGAATCCAAAGACTTTCACCTTCTACCGGCGGACATGGGGTTCACCTCCAGCT	360
Db	338	GTGCCAAGGAATCCAAAGACTTTCACCTTCTACCGGCGGACATGGGGTTCACCTCCAGCT	397
QY	361	TCGAGTCCGGCTGCCTACCGGGGCTGGTTCCTGTGCAAGGTGCTGAAGCCGATCAGCCGTG	420
Db	398	TCGAGTCCGGCTGCCTACCGGGGCTGGTTCCTGTGCAAGGTGCTGAAGCCGATCAGCCGTG	457
QY	421	TCAGACTCACCCAGCTTCCCGAGAAATGGGTGGAAATGCCCCATCAAGACTTCTACT	480
Db	458	TCAGACTCACCCAGCTTCCCGAGAAATGGGTGGAAATGCCCCATCAAGACTTCTACT	517
QY	481	TCAGAGTGTGTACTAGGCGAACGTGCCCGCCCGGAACTCCCTGGGCGAGCGAGCTCGG	540
Db	518	TCAGAGTGTGTACTAGGCGAACGTGCCCGCCCGGAACTCCCTGGGCGAGCGAGCTCGG	576
QY	541	GTGAGGGGTGAGTGGAGAGACCCATGGCGGCAATCACTTCTGCTCTCAGGACCCC	600
Db	577	GTGAGGGGTGAGTGGAGAGACCCATGGCGGCAATCACTTCTGCTCTCAGGACCCC	636
QY	601	CAGGCTCTGACTTAGTGGGCACTGACCACTTTGTCTTCTGGTTCCCGAGTTTGCATAAAT	660
Db	637	CAGGCTCTGACTTAGTGGGCACTGACCACTTTGTCTTCTGGTTCCCGAGTTTGCATAAAT	696
QY	661	CTGAGATTTGGAGCTCAGTCCAGGTCCTCCCGCACTGGAGTGGTGTCTGCTGTGGAAC	720
Db	697	CTGAGATTTGGAGCTCAGTCCAGGTCCTCCCGCACTGGAGTGGTGTCTGCTGTGGAAC	756
QY	721	CTTTGTAATAACCATGTGGGGTAACTGGGNAATCAATGAAGATTTCTGTGGGGTGGG	780
Db	757	CTTTGTAATAACCATGTGGGGTAACTGGGNAATCAATGAAGATTTCTGTGGGGTGGG	816
QY	781	GTGGGGAGTGTGGGAATCATTTCTCTTAAATGGTAACTGCAAGTGTACCCCTGAGCC	840
Db	817	GTGGGGAGTGTGGGNAATCATTTCTCTGTAAATGGTAACTGCAAGTGTACCCCTGAGCC	876
QY	841	CCGACGCCAACCCATCCCGAGTTCAGTTCATAGGGTTCAGTGTCTCCACATGAAGTC	900
Db	877	CCGACGCCAACCCATCCCGAGTTCAGTTCATAGGGTTCAGTGTCTCCACATGAAGTC	936
QY	901	CTCTCACTCAACCATGTGACGAGAGAGGAGTGTATAGGTCAGTGATGATGAGGAT	960
Db	937	CTCTCACTCAACCATGTGACGAGAGAGGAGTGTATAGGTCAGTGATGATGAGGAT	996
QY	961	TGGCCACAGCCCGCCCTTTCCCTTT-ATCCTGCCACTGTATATGCTACCTTTCCCTATC	1019
Db	997	TGGCCACAGCCCGCCCTTTCCCTTTAACTCTGCCACTGTATATGCTACCTTTCCCTATC	1056
QY	1020	TCCTTCCCTCATCATCTTTGTTGTGGGCATAGAGGAGTGGTGAATGTCAAGAAATGGTTCG	1079
Db	1057	TCCTTCCCTCATCATCTTTGTTGTGGGCATAGAGGAGTGGTGAATGTCAAGAAATGGTTCG	1116
QY	1080	AGCTCAGAAGATAAAGATAAGTAGGTAATGCTGATCTCTTTTAAACCCCAAGATACA	1139
Db	1117	AGCTCAGAAGATAAAGATAAGTAGGTAATGCTGATCTCTTTTAAACCCCAAGATACA	1176
QY	1140	ATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAGAGTGTCTCATGACATATGAGAA	1199
Db	1177	ATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAGAGTGTCTCATGACATATGAGAA	1236
QY	1200	GACCTACTTAAAGAGTGGCATATATGCAATTTATTTTAAATAAGATACCTATTATTA	1259
Db	1237	GACCTACTTAAAGAGTGGCATATATGCAATTTATTTTAAATAAGATACCTATTATTA	1296
QY	1260	TATTTCTTTATAGAAAAGTCTGGAAGAGTTTCAATTTGAGCAATGTGAGGGTGG	1319
Db	1297	TATTTCTTTATAGAAAAGTCTGGAAGAGTTTCAATTTGAGCAATGTGAGGGTGG	1356

QY	1320	TGGCAGTATAGGTGATTTTCTTTAAATTCGTTAAATTTATCTGATTTCTCTAATTTTC	1379
Db	1357	TGGCAGTATAGGTGATTTTCTTTAAATTCGTTAAATTTATCTGATTTCTCTAATTTTC	1416
QY	1380	TACATGAAGATGAATTCCTTGTATATAAAATAAGAAAGAAATTAATCTTCAGGTAAAGCA	1439
Db	1417	TACATGAAGATGAATTCCTTGTATATAAAATAAGAAAGAAATTAATCTTCAGGTAAAGCA	1476
QY	1440	GAGCAGACATCATCTCTGATTTGCTCCTCAGCCTCCAAATTCCTCCAGAGTAAATTCAAATGA	1499
Db	1477	GAGCAGACATCATCTCTGATTTGCTCCTCAGCCTCCAAATTCCTCCAGAGTAAATTCAAATGA	1536
QY	1500	ATCGAGCTCTGCTGCTCTGCTGTTGTTGTTAGTAGTATCAGGAAACAGATCTCAGCAAGC	1559
Db	1537	ATCGAGCTCTGCTGCTCTGCTGTTGTTGTTAGTAGTATCAGGAAACAGATCTCAGCAAGC	1596
QY	1560	CACCTAGCAGAGAGGCTGCTGAGTTTGTGTGGTGGAAATCTCTGGGTAAAGAACTTAA	1619
Db	1597	CACCTAGCAGAGAGGCTGCTGAGTTTGTGTGGTGGAAATCTCTGGGTAAAGAACTTAA	1656
QY	1620	GAAACAAAATCATCTGTTAAATTTCTTCTAGAAGATCAGAGCCCTGGGATTCAGAGC	1679
Db	1657	GAAACAAAATCATCTGTTAAATTTCTTCTAGAAGATCAGAGCCCTGGGATTCAGAGC	1716
QY	1680	ATTGATCCAGTCTCTAAGAGGCTGCTGATGTTGTTGAATTTGTTGAGATAAGGTCTCTCAGATGTAG	1739
Db	1717	ATTGATCCAGTCTCTAAGAGGCTGCTGATGTTGTTGAATTTGTTGAGATAAGGTCTCTCAGATGTAG	1776
QY	1740	CATCTCTCTTGGAACTCTCAGTCTGTGAGTCTTATTTGGAGATAAGGTCTCTCAGATGTAG	1799
Db	1777	CATCTCTCTTGGAACTCTCAGTCTGTGAGTCTTATTTGGAGATAAGGTCTCTCAGATGTAG	1836
QY	1800	TTAGTTAAAGACAAGTCTATGCTGGATGAAGGTGAGACCTTAAATTTCAATATGATCTGTTTCC	1859
Db	1837	TTAGTTAAAGACAAGTCTATGCTGGATGAAGGTGAGACCTTAAATTTCAATATGATCTGTTTCC	1896
QY	1860	TTGATATAAAGGAGAGACACACAGACAGAGGAGACCGGGGAGAGATATGTAAGATG	1919
Db	1897	TTGATATAAAGGAGAGACACACAGACAGAGGAGACCGGGGAGAGATATGTAAGATG	1956
QY	1920	TAAGCAGAGATCGGAGTTTTCAGCCACAAAGCTAAGAAACACCAAGGATTTGGCAACCA	1979
Db	1957	TAAGCAGAGATCGGAGTTTTCAGCCACAAAGCTAAGAAACACCAAGGATTTGGCAACCA	2016
QY	1980	TCAGAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGCTTTAGAGGATTAACGGC	2039
Db	2017	TCAGAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGCTTTAGAGGATTAACGGC	2076
QY	2040	TCCTGTGAACCTTAAATCTCAGACTTCCAGCCTCTGAAACGAAGAAAGATAATTTTCGG	2099
Db	2077	TCCTGTGAACCTTAAATCTCAGACTTCCAGCCTCTGAAACGAAGAAAGATAATTTTCGG	2136
QY	2100	CTGTTTAAAGCCACCAAGGATAATTTGGTTTACAGCAGCTCTAGGAAACTAATACAGTGT	2159
Db	2137	CTGTTTAAAGCCACCAAGGATAATTTGGTTTACAGCAGCTCTAGGAAACTAATACAGTGT	2196
QY	2160	AAAATGATCCCTGTCTCTCTGTTTAAATTTCTGTTGTTGTTCCCTCCACAAATGTACCA	2219
Db	2197	AAAATGATCCCTGTCTCTCTGTTTAAATTTCTGTTGTTGTTCCCTCCACAAATGTACCA	2256
QY	2220	AAATTTGTTTGTGACCCCAATAGAAATATGGCAGAGTATGTCATGCCACTTCCAAAGAT	2279
Db	2257	AAATTTGTTTGTGACCCCAATAGAAATATGGCAGAGTATGTCATGCCACTTCCAAAGAT	2315
QY	2280	AGTTTATAAAGACACTGACGCTTCTACTTTAGCCCTCTCTCTGTCACCCACCGCC	2339
Db	2316	AGTTTATAAAGACACTGACGCTTCTACTTTAGCCCTCTCTCTGTCACCCACCGCC	2375
QY	2340	CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGTGTGCTGCTATGATGAGGAGCTTA	2399
Db	2376	CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGTGTGCTGCTATGATGAGGAGCTTA	2435
QY	2400	TAAAGAGACTTAGCTGTTAAATAATGAAGTCTCTCTGCCACACAGCCACATTAGTGAACCTA	2459

Db 2436 TAAAGAGACTTACGTGGTAAATAATGAGTCTCTCCACACCCACATAGTGAACCTA 2495
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTAAAGTTCCTCAGTTTGGTCT 2519
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTAAAGTTCCTCAGTTTGGTCT 2555
Qy 2520 AACTTGTATTGAGCAATAGATAAATAATATGAGAGAAAGAG 2562
Db 2556 AACTTGTATTGAGCAATAGATAAATAATATGAGAGAAAGAG 2598

RESULT 5
ABL95718
ID ABL95718 standard; cDNA; 2598 BP.
AC ABL95718;
DT 19-JUL-2002 (first entry)
XX Human angiogenesis related cDNA PRO4342 SEQ ID NO: 315.
DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
XX
XX 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 17-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-0080706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (HILL/) HILLAN K J.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR P-PSDB; ABB95580.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 315; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
Query Match 98.1%; Score 2514.2; DB 6; Length 2598;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
Qy 1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGTTCCGAA 60
Db 38 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGTTCCGAA 97
Qy 61 TGAAGACTCGGCATTTGAAGTGGCTTTATCTGCATTAATACCAGCTTCTAGCTGGAGGC 120
Db 98 TGAAGACTCGGCATTTGAAGTGGCTTTATCTGCATTAATACCAGCTTCTAGCTGGAGGC 157
Qy 121 TGCATGCAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 180
Db 158 TGCATGCAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 217
Qy 181 ATGCCAGCTGTCCCGCGTCACTCTGGGTGTCCAGGGTGAAGCCAGTGCCTGTCATGTG 240
Db 218 ATGCCAGCTGTCCCGCGTCACTCTGGGTGTCCAGGGTGAAGCCAGTGCCTGTCATGTG 277
Qy 241 GGGTGGGCGAGGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
Db 278 GGGTGGGCGAGGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337
Qy 301 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGGGGGAGACATGGGGCTCACCTCCAGCT 360
Db 338 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGGGGGAGACATGGGGCTCACCTCCAGCT 397
Qy 361 TCGAGTCGCTGCCTACCCGGGCTGTTCTCTGTGACCGTGTGCTGAAGCCGATCAGCCTG 420
Db 398 TCGAGTCGCTGCCTACCCGGGCTGTTCTCTGTGACCGTGTGCTGAAGCCGATCAGCCTG 457
Qy 421 TCAGACTACCCAGCTTCCCGAGATGTGGCTGGATGCCCCCATCATCAGAGCTTCTACT 480

Db 458 TCAGACTACCCAGCTTCCCGAGATGGTGGCTGGAATGCCCCCATCAGACACTTCTACT 517
 Qy 481 TCCAGCAGTGTGACTAGAGCAACGTGCCCCCCCCAGAACTCCCTGGGCHAGGCCACTCGG 540
 Db 518 TCCAGCAGTGTGACTAGGCAACGTTG - CCCCCAGAACTCCCTGGGCHAGGCCACTCGG 576
 Qy 541 GTGAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTCTTCTGTCTCTCAGAACCCC 600
 Db 577 GTGAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTCTTCTGTCTCTCAGAACCCC 636
 Qy 601 CAGGTCTGACTTAGTGGGCACTGACCACTTTGTCTTCTGGTTCACAGTTGTCATAAATT 660
 Db 637 CAGCTCTGACTTAGTGGGCACTGACCACTTTGTCTTCTGGTTCACAGTTTGGATAAATT 696
 Qy 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCCCACTGATGGTCTACTGTGTGGAAC 720
 Db 697 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCCCACTGATGGTCTACTGTGTGGAAC 756
 Qy 721 CTTGTAAACCAATGTGGGTAACTGGGAATAACAATGAAAGATTCTGTGGGGGTGG 780
 Db 757 CTTGTAAACCAATGTGGGTAACTGGGAATAACAATGAAAGATTCTGTGGGGGTGG 816
 Qy 781 GTGGGGAGTGTGGGAATCACTCTGCTTAATGTTAACTGAACAAGTGTACCTGAGCC 840
 Db 817 GTGGGGAGTGTGGGAATCACTCTGCTTAATGTTAACTGAACAAGTGTACCTGAGCC 876
 Qy 841 CCGAGGCCAACCCATCCCACTGAGCTTATAGGCTCAGTGTCTCCACATGAAGTC 900
 Db 877 CCGAGGCCAACCCATCCCACTGAGCTTATAGGCTCAGTGTCTCCACATGAAGTC 936
 Qy 901 CTCTCACTCACTGTGAGGAGAGGGAGTGGTCAATAGAGTCAGGGATCTATGGCCCT 960
 Db 937 CTGTCACTCACTGTGAGGAGAGGGAGTGGTCAATAGAGTCAGGGATCTATGGCCCT 996
 Qy 961 TGGCCAGCCCAACCCCTTCCCTTT - ATCCGCACTGTGATATGCTACCTTCTCTATC 1019
 Db 997 TGGCCAGCCCAACCCCTTCCCTTTAACTCCGCACTGTGATATGCTACCTTCTCTATC 1056
 Qy 1020 TCTTCCCTCATCTCTGTGTGGCATAGAGAGTGGTGTATCTCAGAAAGAAATGTTCTG 1079
 Db 1057 TCTTCCCTCATCTCTGTGTGGCATAGAGAGTGGTGTATCTCAGAAAGAAATGTTCTG 1116
 Qy 1080 AGCTCAGAAGATAAAGATAAGTAGGATGCTGATCCTCTTTTAAACCCCAAGATACA 1139
 Db 1117 AGCTCAGAAGATAAAGATAAGTAGGATGCTGATCCTCTTTTAAACCCCAAGATACA 1176
 Qy 1140 ATCAAAATCCAGATGCTGCTCTATCCCATGAAGAAAGTCTCATGATATTCAGAA 1199
 Db 1177 ATCAAAATCCAGATGCTGCTCTATTCCTCATGAAGAAAGTCTCATGATATTCAGAA 1236
 Qy 1200 GACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAATAAAGATACCTATTATA 1259
 Db 1237 GACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAATAAAGATACCTATTATA 1296
 Qy 1260 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGAGCAATGTGAGGGTGG 1319
 Db 1297 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGAGCAATGTGAGGGTGG 1356
 Qy 1320 TGGCAGTATAGGTGATTTTCTTTTAACTCTGTTTAAATTTATCTGATTTCTTAAATTTTC 1379
 Db 1357 TGGCAGTATAGGTGATTTTCTTTTAACTCTGTTTAAATTTATCTGATTTCTTAAATTTTC 1416
 Qy 1380 TACAATGAAGATGAATCTCTGTATATAAATAAAGAAAGAAATTAATCTTGAGTAAGCA 1439
 Db 1417 TACAATGAAGATGAATCTCTGTATATAAATAAAGAAAGAAATTAATCTTGAGTAAGCA 1476
 Qy 1440 GAGCAGACATCATCTCTGATTTGCTCTCAGCTTCCAAATTTCCCAAGATTAATTCAAATTGA 1499
 Db 1477 GAGCAGACATCATCTCTGATTTGCTCTCAGCTTCCCAAGATTAATTCAAATTGA 1536
 Qy 1500 ATCGAGCTCTGCTGCTGCTGTTGGTTGGTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1559
 Db 1537 ATCGAGCTCTGCTGCTGCTGCTGTTGGTTGGTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1596

Qy 1560 CACTGAGGAGGAGCTGTGCTGAGTTTGTGTGCTGGAATCTCTGGGTAGGAACCTTAA 1619
 Db 1597 CACTGAGGAGGAGCTGTGCTGAGTTTGTGTGCTGGAATCTCTGGGTAGGAACCTTAA 1656
 Qy 1620 GAACAAAAATCATCTGTGTAATTTCTTCTTAGAAGGATCAGAGCCCTGGGATTTCCAAGGC 1679
 Db 1657 GAACAAAAATCATCTGTGTAATTTCTTCTTAGAAGGATCAGAGCCCTGGGATTTCCAAGGC 1716
 Qy 1680 ATTGGATCCAGTCTCTAAGAAAGCTGTGCTACTGGTTGAAATTTGTCTCCCTCAAAATTC 1739
 Db 1717 ATTGGATCCAGTCTCTAAGAAAGCTGTGCTACTGGTTGAAATTTGTCTCCCTCAAAATTC 1776
 Qy 1740 CATCTCTTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGCGAGATGAG 1799
 Db 1777 CATCTCTTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGCGAGATGAG 1836
 Qy 1800 TTAGTTAAGACAAAGTCTATGCTGATGAAGGTAGACCTTAAATTCATATGACTGGTTTCC 1859
 Db 1837 TTAGTTAAGACAAAGTCTATGCTGATGAAGGTAGACCTTAAATTCATATGACTGGTTTCC 1896
 Qy 1860 TTGTATGAAGAGGAGAGACACAGAGACAGAGAGACGCGGGGAAGACTATGTAAGATG 1919
 Db 1897 TTGTATGAAGAGGAGAGACACAGAGACAGAGAGACGCGGGGAAGACTATGTAAGATG 1956
 Qy 1920 AAGCAGAGATCGGAGTTTTCAGCCACAGCTAAGAAACACCAAGGATTTGTGCGCAACCA 1979
 Db 1957 AAGCAGAGATCGGAGTTTTCAGCCACAGCTAAGAAACACCAAGGATTTGTGCGCAACCA 2016
 Qy 1980 TCAGAGCTTGGAGAGCAAGAAAGAAATCTTCCCTAGAGCTTTTAGAGGGATAAGCGGC 2039
 Db 2017 TCAGAGCTTGGAGAGCAAGAAAGAAATCTTCCCTAGAGCTTTTAGAGGGATAAGCGGC 2076
 Qy 2040 TCTGTGAAACCTTAAATCTCAGACTTCCAGCTCTGAGCAAGAAAGAAATTTTCGG 2099
 Db 2077 TCTGTGAAACCTTAAATCTCAGACTTCCAGCTCTGAGCAAGAAAGAAATTTTCGG 2136
 Qy 2100 CTGTTTTAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAAACCTTAATACAGCTGCT 2159
 Db 2137 CTGTTTTAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAAACCTTAATACAGCTGCT 2196
 Qy 2160 AAAATGATCCCTGTCTCTCGTGTGTTTACATTTCTGTGTGTGCTCCCTCCCAATGTACCA 2219
 Db 2197 AAAATGATCCCTGTCTCTCGTGTGTTTACATTTCTGTGTGTGCTCCCTCCCAATGTACCA 2256
 Qy 2220 AAGTTGTCTTTGTGACCAATAGAAATATGGCAAGTATGGCATGCCACTTCCAAGATT 2279
 Db 2257 AAGTTGTCTTTGTGA - CCAATAGAAATATGGCAGAGTATGGCATGCCACTTCCAAGATT 2315
 Qy 2280 AGTTTATAAAGACACTCGAGCTTCTAGAGCCCTCTCTCTGCGCACCCACCGCCCC 2339
 Db 2316 AGTTTATAAAGACACTCGAGCTTCTAGAGCCCTCTCTCTGCGCACCCACCGCCCC 2375
 Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAGCTAGCTGCCATCTATGAGCAGGCCTA 2399
 Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAGCTAGCTGCCATCTATGAGCAGGCCTA 2435
 Qy 2400 TAAAGAGACTTACGTGGTAAATAAAGTCTTCCGCCACAGCCACATTAAGTAACCTA 2459
 Db 2436 TAAAGAGACTTACGTGGTAAATAAAGTCTTCCGCCACAGCCACATTAAGTAACCTA 2495
 Qy 2460 GAAGCAGACACTCTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTTGGTCT 2519
 Db 2496 GAAGCAGACACTCTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTTGGTCT 2555
 Qy 2520 AACTGTTTATGCAACATAGATAAATAATATGAGAGAAAGAG 2562
 Db 2556 AACTGTTTATGCAACATAGATAAATAATATGAGAGAAAGAG 2598

XX AC ACAA1239;
XX DT 11-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO4342 cDNA.
XX DE Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX OS Homo sapiens.
XX PN US2003018173-A1.
XX PD 23-JAN-2003.
XX PF 01-MAY-2002; 2002US-00063515.
XX PR 06-DEC-2001; 2001US-00006867.
XX PA (GETH) GENENTECH INC.
XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-401702/38.
DR P-PSDB; ABU90951.
XX
XX New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
XX Disclosure; Fig 151; 345pp; English.
XX
XX The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
XX Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
XX
XX Query Match 98.1%; Score 2514.2; DB 8; Length 2598;
XX Best Local Similarity 99.6%; Pred. No. 0;
XX Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
XX
XX 1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGGCTGCTCCGAA 60
XX DB 38 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGGCTGCTCCGAA 97
XX
XX 61 TGAAGGACTCGGCAATGAAGGTGCTTTATCTGCATAATAACAGCTTCTAGCTGGAGGC 120
XX DB 98 TGAAGGACTCGGCAATGAAGGTGCTTTATCTGCATNATAACAGCTTCTAGCTGGAGGC 157
XX
XX 121 TGCATGCGAGGAGGTCATTAAAGGTGAAGAGATCAGCGTGTGCCCAATCGGTGGCTGG 180
XX DB 158 TGCATGCGAGGAGGTCATTAAAGGTGAAGAGATCAGCGTGTGCCCAATCGGTGGCTGG 217
XX
XX 181 ATGCCAGCTGTCCTCCCGTCATCTGGGTGTCAGGCTGGAAGCCAGTCCCTGTCTATGTG 240
XX DB 218 ATGCCAGCTGTCCTCCCGTCATCTGGGTGTCAGGCTGGAAGCCAGTCCCTGTCTATGTG 277
XX
XX 241 GGGTGGGCGAGGAGCGGCTCTTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
XX DB 278 GGGTGGGCGAGGAGCGGCTCTTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337

QY 301 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACGGCGGGACATGGGGCTCACCTCCAGCT 360
DB 338 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACGGCGGGACATGGGGCTCACCTCCAGCT 397
QY 361 TCGAGTCGGCTCGCTTACACCGGGCTGGTTCCTGTGCACGGTGGCTGAAGCGCATCAGCCTG 420
DB 398 TCGAGTCGGCTCGCTTACACCGGGCTGGTTCCTGTGCACGGTGGCTGAAGCGCATCAGCCTG 457
QY 421 TCAGACTACCCAGCTTCCCGAGAAATGFGGCTGGAATGCCCCCATCACAGACTTCTACT 480
DB 458 TCAGACTACCCAGCTTCCCGAGAAATGFGGCTGGAATGCCCCCATCACAGACTTCTACT 517
QY 481 TCCAGCAGTGTGACTAGGCAACGTCGCCCCCGAGAACTCCCTGGCGAGCCAGCTCGG 540
DB 518 TCCAGCAGTGTGACTAGGCAACGTCGCCCCCGAGAACTCCCTGGCGAGCCAGCTCGG 576
QY 541 GTGAGGGGTGAGTGGAGAGAGACCCATGGCGGACAATCACTTCTTCTGCTCTCAGGACCCC 600
DB 577 GTGAGGGGTGAGTGGAGAGAGACCCATGGCGGACAATCACTTCTTCTGCTCTCAGGACCCC 636
QY 601 CAGGTCTGACTTGTAGTGGGCACTGACCACTTTGTCTTCTGTGTTCCAGTTTGCATATAAT 660
DB 637 CACGTCTGACTTGTAGTGGGCACTTGTCTTCTGTGTTCCAGTTTGCATATAAT 696
QY 661 CTGAGATTTGGAGCTCAGTCCAGGCTCCTCCCGCACTGGATGGTCTACTGCTGTGGAAC 720
DB 697 CTGAGATTTGGAGCTCAGTCCAGGCTCCTCCCGCACTGGATGGTCTACTGCTGTGGAAC 756
QY 721 CTTGTAAAAACCATGTGGGTAAATCTGGGAATAACATGAAAGATTTCTGTGGGGTGGG 780
DB 757 CTTGTAAAAACCATGTGGGTAAATCTGGGAATAACATGAAAGATTTCTGTGGGGTGGG 816
QY 781 GTGGGGAGTGTCTGGGAATCATTTCTGCTTAATGTGTAATGTAACAGTGTACCTCAGCC 840
DB 817 GTGGGGAGTGTCTGGGAATCATTTCTGCTTAATGTGTAACAGTGTACCTCAGCC 876
QY 841 CCGCAGGCCCAACCCATCCCACTTGCAGCTTATAGGTGAGTCTCTCCACATGAAGTC 900
DB 877 CCGCAGGCCCAACCCATCCCACTTGCAGCTTATAGGTGAGTCTCTCCACATGAAGTC 936
QY 901 CTCTCACTCACCACCTGTGCAGGAGGAGGTGGTCTATAGAGTCAGGGATCTATGGCCCT 960
DB 937 CTGTCACTCACCACCTGTGCAGGAGGAGGTGGTCTATAGAGTCAGGGATCTATGGCCCT 996
QY 961 TGGCCCGAGCCCAACCCCTTCCCTTT-ATCTGCCACTGTCTATATGCTACCTTTCTATC 1019
DB 997 TGGCCCGAGCCCAACCCCTTCCCTTTAATCTCTCCACTGTCTATGCTACCTTTCTATC 1056
QY 1020 TCTTCCCTCATCTTCTTGTGGGCATGAGAGGTGGTGTCTCAGAGAATGGTTCG 1079
DB 1057 TCTTCCCTCATCTTCTTGTGGGCATGAGAGGTGGTGTCTCAGAGAATGGTTCG 1116
QY 1080 AGCTCAGAAGATAAAGATAAGTAGGTATGCTGATCTCTTTTAAAAACCCCAAGATACA 1139
DB 1117 AGCTCAGAAGATAAAGATAAGTAGGTATGCTGATCTCTTTTAAAAACCCCAAGATACA 1176
QY 1140 ATCAAAATCCCAAGATGCTGCTCTATTTCCCATGAAAAAGTCTCATGATATTCAGAA 1199
DB 1177 ATCAAAATCCCAAGATGCTGCTCTATTTCCCATGAAAAAGTCTCATGATATTCAGAA 1236
QY 1200 GACCTACTTACAAAGTGGCATATATTTTAAATTTTAAATTTTAAAGATACCTATTATA 1259
DB 1237 GACCTACTTACAAAGTGGCATATATTTTAAATTTTAAATTTTAAAGATACCTATTATA 1296
QY 1260 TATTTCTTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAGGGTGG 1319
DB 1297 TATTTCTTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAGGGTGG 1356
QY 1320 TGGCAGTATAGTGTATTTTCTTTTAAATTTCTGTAAATTTTCTGTATTTCTTAATTTTC 1379
DB 1357 TGGCAGTATAGTGTATTTTCTTTTAAATTTCTGTAAATTTTCTGTATTTCTTAATTTTC 1416
QY 1380 TACAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAAGAAATTAATCTTTGAGGTAAAGCA 1439

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Db	1417	TACAAATGAGATGAATCTCTGTATAAAATGAAGAAATTAATCTTCAGGTAAGCA	1476
Qy	1440	GAGCAGACATCATCTCTGATGTCTCAGCCTCCAAATCCCGCAGATTAATCAAAATGA	1499
Db	1477	GAGCAGACATCATCTCTGATGTCTCAGCCTCCAAATCCCGCAGATTAATCAAAATGA	1536
Qy	1500	ATCGAGCTCTGCTCTCTGTTGTTGTTGATGATCAGGAAACAGATCTCAGCAAGC	1559
Db	1537	ATCGAGCTCTGCTCTCTGTTGTTGTTGATGATCAGGAAACAGATCTCAGCAAGC	1596
Qy	1560	CACGTGAGGAGGAGCTGTCTGATGTTGTGTGGCTGGAATCTCTGGTAAAGAACTTAAA	1619
Db	1597	CACGTGAGGAGGAGCTGTCTGATGTTGTGTGGCTGGAATCTCTGGTAAAGAACTTAAA	1656
Qy	1620	GAACAAAATCATCTGGTAATCTCTTCTAGAGGATCACGCCCTCGGATTCGAAGC	1679
Db	1657	GAACAAAATCATCTGGTAATCTCTTCTAGAGGATCACGCCCTCGGATTCGAAGC	1716
Qy	1680	ATTGGATCCAGTCTCTAAGAAAGCTGCTGATCTGTTGAAATGTGTCCCTCAAAATCA	1739
Db	1717	ATTGGATCCAGTCTCTAAGAAAGCTGCTGATCTGTTGAAATGTGTCCCTCAAAATCA	1776
Qy	1740	CATCCTTCTTGGAAATCTCAGTCTGTGATTTATTTGGAGATTAAGCTCTCGAGATGAG	1799
Db	1777	CATCCTTCTTGGAAATCTCAGTCTGTGATTTATTTGGAGATTAAGCTCTCGAGATGAG	1836
Qy	1800	TTAGTTAAGCAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATATGACTGGTTCC	1859
Db	1837	TTAGTTAAGCAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATATGACTGGTTCC	1896
Qy	1860	TTGTATGAAAAGGAGAGACACAGAGACAGAGAGACGGGGAGACACTATGTAAGATG	1919
Db	1897	TTGTATGAAAAGGAGAGACACAGAGACAGAGAGACGGGGAGACACTATGTAAGATG	1956
Qy	1920	AAGCAGAGATCGAGTTTTCAGCCACAGCTTAAGAAACACCAAGGATTTGGCAACCA	1979
Db	1957	AAGCAGAGATCGAGTTTTCAGCCACAGCTTAAGAAACACCAAGGATTTGGCAACCA	2016
Qy	1980	TCAGAAAGCTTGAAGAGCAAGAAAGAAATCTTCCCTAGAGCTTTAGAGGATTAACGC	2039
Db	2017	TCAGAAAGCTTGAAGAGCAAGAAAGAAATCTTCCCTAGAGCTTTAGAGGATTAACGC	2076
Qy	2040	TCTGCTGAACTTAACTCTCAGCTCCAGCTCTGAAAGAAAGAAATTAATTTCCG	2099
Db	2077	TCTGCTGAACTTAACTCTCAGCTCCAGCTCTGAAAGAAAGAAATTAATTTCCG	2136
Qy	2100	CTGTTTAAAGCACCAGCAAGTAAATGGTTACAGAGCTCTAGGAACTAATACAGTGT	2159
Db	2137	CTGTTTAAAGCACCAGCAAGTAAATGGTTACAGAGCTCTAGGAACTAATACAGTGT	2196
Qy	2160	AAAAATGATCCCTCTCTCTGTTTACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2219
Db	2197	AAAAATGATCCCTCTCTCTGTTTACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2256
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Db	2436	TAAAGAGACTTACGTGGTAAAAAATGAAGTCTCTCTGCCCCCAGCCACATTTAGTGAACCTA	2495
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Qy 2520 AACTTGTATGAGCAATAGATAAATAATATCAGAGAAAGAG 2562
Db 2556 AACTTGTATGAGCAATAGATAAATAATATCAGAGAAAGAG 2598
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RESULT 10

ACA64061
ID ACA64061 standard; cDNA; 2598 BP.

XX ACA64061;

XX AC

XX 16-JUN-2003 (first entry)

XX cDNA encoding human PRO polypeptide #76.

XX XX

KW Human; PRO polypeptide; secreted and transmembrane protein;

XX anti-PRO antibody; diagnostic assay; gene expression; gene; ss.

OS Homo sapiens.

XX XX

PN US2002182638-A1.

XX XX

PD 05-DEC-2002.

XX XX

PF 02-MAY-2002; 2002US-00063547.

XX XX

PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 01-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX P-PSDB; ABU72362.
XX WPI; 2003-328612/04.
DR DR
DR DR
XX PT
XX PT
XX PS
XX PS
XX PS
XX The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of a condition responsive to anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. CC AC63986-ACA64069 represent cDNA sequences encoding the human PRO polypeptides of the invention
XX Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
SQ
Query Match 98.1%; Score 2514.2; DB 8; Length 2598;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
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DB 38 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGCTTCGGAA 97
QY 61 TGAAGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 120
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DB 98 TGAAGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 157
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DB 1477 GAGCAGACATCATCTGATTCCTCAGCTCCCAATTCGCCAGAGTAATTCAAATTTGA 1536
QY 1500 ATCGAGCTCTGCTGCTCTGTTGGTTGTAGTAGTATCAGGAAAAAGATCTCAGCAAAAGC 1559
DB 1537 ATCGAGCTCTGCTGCTCTGTTGGTTGTAGTAGTATCAGGAAAAAGATCTCAGCAAAAGC 1596
QY 1560 CACTGAGGAGGAGGCTGCTGAGTTTGTGTGGTGAATCTCTGGGTAAAGAACTTAAA 1619
DB 1597 CACTGAGGAGGAGGCTGCTGAGTTTGTGTGGTGAATCTCTGGGTAAAGAACTTAAA 1656
QY 1620 GAACAAAAATCATCTGTAATTTCTTCCCTAGAAAGATCAAGCCCTGGGATTCAGAGC 1679
DB 1657 GAACAAAAATCATCTGTAATTTCTTCCCTAGAAAGATCAAGCCCTGGGATTCAGAGC 1716
QY 1680 ATTGATCCAGTCTCTAAGAGGCTGCTGATCTGTTGAATTTGTGTCCTCCCTCAAAATTC 1739
DB 1717 ATTGATCCAGTCTCTAAGAGGCTGCTGATCTGTTGAATTTGTGTCCTCCCTCAAAATTC 1776
QY 1740 CATCTCTTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1799
DB 1777 CATCTCTTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1836
QY 1800 TTAGTTAAGCAAGGTCATCTGGATGAAGGTAGACCTAAATCAATATGACTGTTTCC 1859
DB 1837 TTAGTTAAGCAAGGTCATCTGGATGAAGGTAGACCTAAATCAATATGACTGTTTCC 1896
QY 1860 TTGTATGAAGAGGAGGACACAGACAGAGAGGAGCGGGGAGACTATGTAAAGATG 1919
DB 1897 TTGTATGAAGAGGAGGACACAGACAGAGAGGAGCGGGGAGACTATGTAAAGATG 1956
QY 1920 AAGGCAGAGATCGGAGTTTTCAGGCCACAAGCTTAAGAAAACCAAGGATTTGGCAACCA 1979
DB 1957 AAGGCAGAGATCGGAGTTTTCAGGCCACAAGCTTAAGAAAACCAAGGATTTGGCAACCA 2016
QY 1980 TCAGAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2039
DB 2017 TCAGAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2076
QY 2040 TCTGCTGAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGGAGAAAGATAAATTTCCG 2099
DB 2077 TCTGCTGAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGGAGAAAGATAAATTTCCG 2136
QY 2100 CTGTTTAAAGCACCAGGATTAATTTGGTTTACAGCAGCTCTAGGAAACTAATACAGCTGCT 2159
DB 2137 CTGTTTAAAGCACCAGGATTAATTTGGTTTACAGCAGCTCTAGGAAACTAATACAGCTGCT 2196
QY 2160 AAAATGATCCCTGTCTCTCGTGTGTTTACATTTCTGTGTGTGTCCCTCCACCAATGTACCA 2219
DB 2197 AAAATGATCCCTGTCTCTCGTGTGTTTACATTTCTGTGTGTGTCCCTCCACCAATGTACCA 2256
QY 2220 AAGTTCTCTTTGTGACCCCAATAGATATGCGAGAGTGTGGCATGCCACTTCCAGATT 2279
DB 2257 AAGTTCTCTTTGTGA-CCAATAGATATGCGAGAGTGTGGCATGCCACTTCCAGATT 2315

QY 2280 AGTTTATAAAGACACTGCAGCTTCTACTTTAGCCCTCTCTCTGCGCACCCACCGCCCC 2339
DB 2316 AGTTTATAAAGACACTGCAGCTTCTACTTTAGCCCTCTCTCTGCGCACCCACCGCCCC 2375
QY 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAAAGCTAGCTGCGCATGTATGAGCAGGCCTA 2399
DB 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAAAGCTAGCTGCGCATGTATGAGCAGGCCTA 2435
QY 2400 TAAAGAGACTTACGTGGTAAAAAAATGAAGTCTCTGCGCCACAGCCACATTAGTGAACCTA 2459
DB 2436 TAAAGAGACTTACGTGGTAAAAAAATGAAGTCTCTGCGCCACAGCCACATTAGTGAACCTA 2495
QY 2460 GAAGCAGACACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519
DB 2496 GAAGCAGACACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555
QY 2520 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562
DB 2556 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2598

RESULT 11
ACA91325
ID ACA91325 standard; cdna; 2598 BP.
XX
AC ACA91325;
XX
DT 14-JUL-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #76.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003018168-A1.
XX
PD 23-JAN-2003.
XX
PF 02-MAY-2002; 2002US-00063569.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 15-SEP-1999; 99US-00380142.
PR 18-OCT-1999; 99US-00397342.
PR 12-NOV-1999; 99US-00403297.
PR 30-DEC-1999; 99US-00423844.
PR 18-FEB-2000; 99WO-US031274.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 24-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX (GETH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-401699/38.
DR P-PSDB; ABU91035.
XX
XX New isolated, secreted and transmembrane PRO polypeptide, useful for the
PT diagnosis, prevention and treatment of rectal, lung, stomach, esophageal
PT or skin cancers.
XX
XX Disclosure; Fig 151; 235pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO polypeptide
CC and polynucleotide sequences are useful for the diagnosis, prevention and
CC treatment of rectal, lung, stomach, oesophageal or skin tumours, and/or
CC cancers. The PRO polypeptides are also useful as molecular weight
CC markers. The PRO polynucleotide sequences are useful for chromosome
CC identification, hybridisation probes, and for screening libraries of
CC human cDNA, genomic DNA or mRNA. They may also be used in gene therapy,
CC particularly for replacing a defective gene. ACA91250-ACA91333 represent
CC cDNA sequences encoding the human PRO polypeptides of the invention
XX
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match 98.1%; Score 2514.2; DB 8; Length 2598;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

QY 1 AGGGAGTCTACCCCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGTGTCTCCGAA 60
DB 38 AGGGAGTCTACCCCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGTGTCTCCGAA 97
QY 61 TGAAGGACTCGGCATTGAAGTGTCTTATCTGATAATAACAGCTTCTAGCTGGAGGCG 120
DB 98 TGAAGGACTCGGCATTGAAGTGTCTTATCTGATAATAACAGCTTCTAGCTGGAGGCG 157
QY 121 TGCATGCAAGGAGGTCATTAAAGGTGAAGAGATCAGCGTGTGCCCAATCGGTGGCTGG 180
DB 158 TGCATGCAAGGAGGTCATTAAAGGTGAAGAGATCAGCGTGTGCCCAATCGGTGGCTGG 217
QY 181 ATGCAGCCTGTCCCCCGTCATCTGGGTGTCCAGGTGGAAGCCAGTGCCTGTATGTG 240
DB 218 ATGCAGCCTGTCCCCCGTCATCTGGGTGTCCAGGTGGAAGCCAGTGCCTGTATGTG 277
QY 241 GGGTGGGCGAGGAGCGAGCTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
DB 278 GGGTGGGCGAGGAGCGAGCTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337
QY 301 GTGCCAAGGAATCCAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT 360
DB 338 GTGCCAAGGAATCCAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT 397
QY 361 TCGAGTGGCTGGCTACCCGGGCTGGTCTGTGACCGGTGCTGAAGCCGATCAGCCTG 420
DB 398 TCGAGTGGCTGGCTACCCGGGCTGGTCTGTGACCGGTGCTGAAGCCGATCAGCCTG 457
QY 421 TCAGACTACCCAGCTTCCCGAGATGGTGGTGAATGCCCCCATCAAGACTTCTACT 480
DB 458 TCAGACTACCCAGCTTCCCGAGATGGTGGTGAATGCCCCCATCAAGACTTCTACT 517
QY 481 TCCAGAGTGTGACTAGGGCAACGTGCCCCCCCCAGAACTCTCCCTGGGCGAGCCAGCTGG 540

DB 518 TCCAGCAGTGTGACTAGGGCAACGTG-CCCCCCAGAACTCCTTGGGCGAGCCAGCTCGG 576
QY 541 GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTCTGTCTCTCAGGACCCC 600
DB 577 GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGTCTCTCAGGACCCC 636
QY 601 CAGGTCTGACTTGTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCTCAGTTTCATAAATT 660
DB 637 CACGTCTGACTTGTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCTCAGTTTCATAAATT 696
QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCACTGGATGGTCTGCTACTGCTGTGGAC 720
DB 697 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCACTGGATGGTCTGCTGTGTGGAAC 756
QY 721 CTTGTAAAAACCATGTGGGTAAACTGGGAATAACATGAAAAAGATTCTCTGTGGGGGTGG 780
DB 757 CTTGTAAAAACCATGTGGGTAAACTGGGAATAACATGAAAAAGATTCTCTGTGGGGGTGG 816
QY 781 GTGGGGGAGTGTCTGGGAATCAATCTCTGCTTAATGTGTAATGTAAGTGTACCTTGAGCC 840
DB 817 GTGGGGGAGTGTCTGGGAATCAATCTCTGCTTAATGTGTAAGTGTACCTTGAGCC 876
QY 841 CCGCAGGCCAACCCATCCCACTTATAGGCTTAGGCTCAGTCTCTCCACATGAAGTC 900
DB 877 CCGCAGGCCAACCCATCCCACTTATAGGCTTAGGCTCAGTCTCTCCACATGAAGTC 936
QY 901 CTCTCACTCACCACATGTGCAGGAGGAGGTGGTGTATAGAGTCAGGGATCTATGGCCCT 960
DB 937 CTGTCACTCACCACATGTGCAGGAGGAGGTGGTGTATAGAGTCAGGGATCTATGGCCCT 996
QY 961 TGGCCCGAGCCCGCCCTTCCCTTT-ATCTGCGCACTGTCTATGCTACTACCTTTCTATC 1019
DB 997 TGGCCCGAGCCCGCCCTTCCCTTTAATCTCTGCACTGTCTATGCTACCTTTCTATC 1056
QY 1020 TCTTCCCTCATCTTGTGTGGGCATGAGAGGTGGTGTGATGTCAGAAGAATGGTTGG 1079
DB 1057 TCTTCCCTCATCTTGTGTGGGCATGAGAGGTGGTGTGATGTCAGAAGAATGGCTCG 1116
QY 1080 AGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTAAAAACCCCAAGATACA 1139
DB 1117 AGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTAAAAACCCCAAGATACA 1176
QY 1140 ATCAAAATCCAGATGTGCTCTATTCCCATGAAAAAGTCTCATGACATATTGAGAA 1199
DB 1177 ATCAAAATCCAGATGTGCTCTATTCCCATGAAAAAGTCTCATGACATATTGAGAA 1236
QY 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTTAAAGATACCTATTATA 1259
DB 1237 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTTAAAGATACCTATTATA 1296
QY 1260 TATTTCTTTATAGAAAAAGTCTGGAAGTTTACTTCAATTTGTAGCAATGTCAAGGTGG 1319
DB 1297 TATTTCTTTATAGAAAAAGTCTGGAAGTTTACTTCAATTTGTAGCAATGTCAAGGTGG 1356
QY 1320 TGGCAGTATAGTGAATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAATTTTC 1379
DB 1357 TGGCAGTATAGTGAATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAATTTTC 1416
QY 1380 TACAATGAAGATGAATTCCTTGTATATAAATAAAGAAAAAATTAATCTTGAGGTAAAGCA 1439
DB 1417 TACAATGAAGATGAATTCCTTGTATATAAATAAAGAAAAAATTAATCTTGAGGTAAAGCA 1476
QY 1440 GAGCAGACATCATCTGATTCCTCAGCCTCCCAATTTCCCGAGAGTAAATTCAAATTCGA 1499
DB 1477 GAGCAGACATCATCTGATTCCTCAGCCTCCCAATTTCCCGAGAGTAAATTCAAATTCGA 1536
QY 1500 ATCGAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1559
DB 1537 ATCGAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1596
QY 1560 CACTGAGGAGGCTGTGCTGAGTTTGTGGCTGGATCTCTGGGTAGGAATCTTCTGGGTAGGA 1619

Db 1597 CACTGAGGAGGCTGTGCTGAGTTTGTGCTGGAATCTCTGGTAAGGAACCTTAA 1656
Qy 1620 GAACAAAAATCATCTGGTAATCTTCTTCCTAGAAAGATCAAGCCCTGGATTCGAAGC 1679
Db 1657 GAACAAAAATCATCTGGTAATCTTCTTCCTAGAAAGATCAAGCCCTGGATTCGAAGC 1716
Qy 1680 ATTGGATCCAGTCTCTAAGAGGCTGCTACTGTTGTAATTTGTCCTCCCTCAATTTCA 1739
Db 1717 ATTGGATCCAGTCTCTAAGAGGCTGCTACTGTTGTAATTTGTCCTCCCTCAATTTCA 1776
Qy 1740 CATCTCTTCTTGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1799
Db 1777 CATCTCTTCTTGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1836
Qy 1800 TTAGTTAAGCAAGGTCATCTGGATGAAGGTAGACCTAAATTCATATGACTGTTTCC 1859
Db 1837 TTAGTTAAGCAAGGTCATCTGGATGAAGGTAGACCTAAATTCATATGACTGTTTCC 1896
Qy 1860 TTGTATGAAGAGGAGGACACAGACAGAGGAGCGGGGAGACTATGTTAAGATG 1919
Db 1897 TTGTATGAAGAGGAGGACACAGACAGAGGAGCGGGGAGACTATGTTAAGATG 1956
Qy 1920 AAGGCAGAGATCGGAGTTTTCAGGCCCAAGCTTAAGAAACACCAAGATTTGGCAACCA 1979
Db 1957 AAGGCAGAGATCGGAGTTTTCAGGCCCAAGCTTAAGAAACACCAAGATTTGGCAACCA 2016
Qy 1980 TCAGAAGCTTGAAGGCAAGAAATTCCTCCTAGAGCTTTAGAGGATTAACGCG 2039
Db 2017 TCAGAAGCTTGAAGGCAAGAAATTCCTCCTAGAGCTTTAGAGGATTAACGCG 2076
Qy 2040 TCTGCTGAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCG 2099
Db 2077 TCTGCTGAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCG 2136
Qy 2100 CTGTTTAAAGCACCAGGATAATTTGTTACAGAGCTCTAGGAACTAATACAGTCT 2159
Db 2137 CTGTTTAAAGCACCAGGATAATTTGTTACAGAGCTCTAGGAACTAATACAGTCT 2196
Qy 2160 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCCAATGTACCA 2219
Db 2197 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCCAATGTACCA 2256
Qy 2220 AAGTTGCTTTGTGACCAATAGATATGGCAGAGTGTGGCATGCCACTTCCAGATT 2279
Db 2257 AAGTTGCTTTGTGA - CCAATAGATATGGCAGAGTGTGGCATGCCACTTCCAGATT 2315
Qy 2280 AGGTTATAAAGACACTGCAGCTTCTACTTGTAGCCCTCTCTCTGCGCACCCACCGCCC 2339
Db 2316 AGGTTATAAAGACACTGCAGCTTCTACTTGTAGCCCTCTCTCTGCGCACCCACCGCCC 2375
Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCGGCTTA 2399
Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCGGCTTA 2435
Qy 2400 TAAAGAGACTTACGTGTTAAAAATAGAGTCTCTGCGCACAGCCACATTAAGTAACCTTA 2459
Db 2436 TAAAGAGACTTACGTGTTAAAAATAGAGTCTCTGCGCACAGCCACATTAAGTAACCTTA 2495
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555
Qy 2520 AACTTGTATGAGCAATAGATAAATAATATATGAGAGAAAGAG 2562
Db 2556 AACTTGTATGAGCAATAGATAAATAATATATGAGAGAAAGAG 2598

RESULT 12
ACD45224

ID ACD45224 standard; cDNA; 2598 BP.

XX AC ACD45224;

XX

DT 11-SEP-2003 (first entry)
XX Human secreted/transmembrane polypeptide PRO4342 cDNA.
XX Human; ss; tumour; cancer; gene therapy; tissue typing; gene.
XX Homo sapiens.

OS US2003009012-A1.

XX 09-JAN-2003.

XX 01-MAY-2002; 2002US-00063517.

XX 30-DEC-1998; 98KR-00062142.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99US-00311832.

XX 14-MAY-1999; 99WO-US010733.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

XX 25-AUG-1999; 99US-00380139.

XX 15-SEP-1999; 99US-00397342.

XX 18-OCT-1999; 99US-00403297.

XX 12-NOV-1999; 99US-00423844.

XX 30-DEC-1999; 99WO-US031274.

XX 18-FEB-2000; 2000WO-US004341.

XX 02-MAR-2000; 2000WO-US005601.

XX 21-MAR-2000; 2000WO-US007532.

XX 22-MAY-2000; 2000WO-US014042.

XX 02-JUN-2000; 2000WO-US015264.

XX 22-AUG-2000; 2000US-00644848.

XX 24-AUG-2000; 2000WO-US023328.

XX 18-SEP-2000; 2000US-00664610.

XX 08-SEP-2000; 2000US-00665350.

XX 08-NOV-2000; 2000US-00709238.

XX 01-DEC-2000; 2000WO-US030873.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 28-FEB-2001; 2001WO-US006520.

XX 22-MAR-2001; 2001US-00816744.

XX 10-MAY-2001; 2001US-00854208.

XX 30-MAY-2001; 2001US-00854280.

XX 01-JUN-2001; 2001WO-US017800.

XX 05-JUN-2001; 2001US-00874503.

XX 29-JUN-2001; 2001US-00869599.

XX 18-JUL-2001; 2001US-00908827.

XX 06-DEC-2001; 2001US-00006867.

(GETH) GENENTECH INC.

Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2003-447383/42.

P-PSDB; ABO27356.

New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.

Dislosure; Fig 151; 223pp; English.

The invention relates to an antibody that binds to a secreted and transmembrane PRO polypeptide. The methods and compositions of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful

CC in the development and screening of therapeutically useful reagents. The
CC PRO polypeptides and encoding nucleic acids can be used as molecular
CC weight markers for protein electrophoresis, chromosome identification and
CC tissue typing. The antibodies may be used in various diagnostic,
CC competitive binding and/or immunoprecipitation assays. The present
CC sequence represents a secreted and transmembrane PRO polypeptide cDNA
xx
SO Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match	98.1%	Score 2514.2	DB 8	Length 2598
Best Local Similarity	99.6%	Pred. NO. 0		
Matches 2552	Conservative	0	Mismatches 8	Indels 3
				Gaps 3

QY	1	AGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAA	60
DB	38	AGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAA	97
QY	61	TGAAGGACTCGGACTTGAAGGTGCTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGC	120
DB	98	TGAAGGACTCGGACTTGAAGGTGCTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGC	157
QY	121	TGCATTCGAGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCCAAATCGGTGGCTGG	180
DB	158	TGCATTCGAGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCCAAATCGGTGGCTGG	217
QY	181	ATGCCAGCGCTGTCCCGCTCATCTCTGGGTGTCAGGGTGGAAAGCAGTGCCTGTCTAATGTG	240
DB	218	ATGCCAGCGCTGTCCCGCTCATCTCTGGGTGTCAGGGTGGAAAGCAGTGCCTGTCTAATGTG	277
QY	241	GGGTGGGCAGAGCGGACTCTAAACATAGAGCCAGTGAACATCATGGAGCTCTATCTTG	300
DB	278	GGGTGGGCAGAGCGGACTCTAAACATAGAGCCAGTGAACATCATGGAGCTCTATCTTG	337
QY	301	GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT	360
DB	338	GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT	397
QY	361	TCGAGTCCGCTGCCTACCCGGCTGGTTCCTGTGCACGGTGCTGAAGCCGATCAGCCCTG	420
DB	398	TCGAGTCCGCTGCCTACCCGGCTGGTTCCTGTGCACGGTGCTGAAGCCGATCAGCCCTG	457
QY	421	TCGAGTCAACCAGCTTCCCGAGATGGTGGCTGGNATGCCGCCCATCAGAGCTTCTACT	480
DB	458	TCGAGTCAACCAGCTTCCCGAGATGGTGGCTGGNATGCCGCCCATCAGAGCTTCTACT	517
QY	481	TCCACGAGTGTCACTAGGCAACGTCGCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCCG	540
DB	518	TCCACGAGTGTCACTAGGCAACGTCGCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCCG	576
QY	541	GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTTGTCTCTCAGGACCCC	600
DB	577	GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGTCTCTCAGGACCCC	636
QY	601	CAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCTCAGTTTGCATAAAT	660
DB	637	CAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCTCAGTTTGCATAAAT	696
QY	661	CTGAGATTGGAGCTCAGTCCAGGTGCTCCCCCACTGATGGTGTCTACTGTGTGGAC	720
DB	697	CTGAGATTGGAGCTCAGTCCAGGTGCTCCCCCACTGATGGTGTCTACTGTGTGGAC	756
QY	721	CTTGTAAAAACCATGTGGGTAAAACTGGGAATAACATGAAGAATTTCTGTGGGGGTGG	780
DB	757	CTTGTAAAAACCATGTGGGTAAAACTGGGAATAACATGAAGAATTTCTGTGGGGGTGG	816
QY	781	GTGGGGAGTGTGGGAATCATTTCTCTGCTTAATGGTAACTGACAAGTGTTAACCTCAGCC	840
DB	817	GTGGGGAGTGTGGGAATCATTTCTCTGCTTAATGGTAACTGACAAGTGTTAACCTCAGCC	876
QY	841	CCGCAAGCCAAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC	900
DB	877	CCGCAAGCCAAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC	936

Qy	901	CTCTCACTCAACCACTGTGCAGGAGAGGGAGGTGGTCAATAGAGTCAGGATCTATGGCCCT	960
Db	937	CTGTCACTCAACCACTGTGCAGGAGAGGGAGGTGGTCAATAGAGTCAGGATCTATGGCCCT	996
Qy	961	TGGCCACGCCCCACCCCTTCCCTTTT-ATCCTGCGCACTGTCATATGCTACTCTTTCCTATC	1019
Db	997	TGGCCACGCCCCACCCCTTCCCTTTTAACTCTGCCACTGTCATATGCTACTCTTTCCTATC	1056
Qy	1020	TCTTCCCTCATCATCTTTGTTGTGGGCATAGGAGGGTGGTCAATGTCAGAGAAATGFTTCG	1079
Db	1057	TCTTCCCTCATCATCTTTGTTGTGGGCATAGGAGGGTGGTCAATGTCAGAGAAATGFTTCG	1116
Qy	1080	AGCTCAGAAGATAAAGATAAGTAGGTATGCTGATCCTCTTTTAAAAACCCCAAGATACA	1139
Db	1117	AGCTCAGAAGATAAAGATAAGTAGGTATGCTGATCCTCTTTTAAAAACCCCAAGATACA	1176
Qy	1140	ATCAAAATCCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCAATGACATATTGAGAA	1199
Db	1177	ATCAAAATCCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCAATGACATATTGAGAA	1236
Qy	1200	GACCTACTTACAAAGTGGCATATATTGCCAATTTATTTTAAATAAAAGATACCTATTTATA	1259
Db	1237	GACCTACTTACAAAGTGGCATATATTGCCAATTTATTTTAAATAAAAGATACCTATTTATA	1296
Qy	1260	TATTTCTTTATAGAAAAAGCTCGGAAGAGTTTACTTCAATTTGAGCAATGTCAGGGTGG	1319
Db	1297	TATTTCTTTATAGAAAAAGCTCGGAAGAGTTTACTTCAATTTGAGCAATGTCAGGGTGG	1356
Qy	1320	TGGCAGTATAGGTGATTTTCTTTTAACTCTGTTTAAATTAATCTGTAATTCCTATTTTTC	1379
Db	1357	TGGCAGTATAGGTGATTTTCTTTTAACTCTGTTTAAATTAATCTGTAATTCCTATTTTTC	1416
Qy	1380	TACAAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAAGAAATTAATCTTGAGGTAAACA	1439
Db	1417	TACAAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAAGAAATTAATCTTGAGGTAAACA	1476
Qy	1440	GAGCAGACATCATCTCTGATTTGCTCAGGCTTCAATTCCTCCAGAGTAAATTCAAATTTGA	1499
Db	1477	GAGCAGACATCATCTCTGATTTGCTCAGGCTTCAATTCCTCCAGAGTAAATTCAAATTTGA	1536
Qy	1500	ATCGAGCTCTGCTGCTCTGGTTGGTGTAGTGTAGTATGATCAGAGAACAGATCTCAGCAAGC	1559
Db	1537	ATCGAGCTCTGCTGCTCTGGTTGGTGTAGTGTAGTATGATCAGAGAACAGATCTCAGCAAGC	1596
Qy	1560	CACGTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGGAATCTTAAA	1619
Db	1597	CACGTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGGAATCTTAAA	1656
Qy	1620	GAACAAAAATCATCTGTAATTTCTTTCCTAGAGGATCAACAGCCCTGGGATTCCAAGGC	1679
Db	1657	GAACAAAAATCATCTGTAATTTCTTTCCTAGAGGATCAACAGCCCTGGGATTCCAAGGC	1716
Qy	1680	ATTGGATCCAGTCTCTAAGAAAGGCTGCTGTACTGTTGAAATTTGTTGCCCTCAGAAATCA	1739
Db	1717	ATTGGATCCAGTCTCTAAGAAAGGCTGCTGTACTGTTGAAATTTGTTGCCCTCAGAAATCA	1776
Qy	1740	CATCCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTTGAGATAAGGCTCTCTGCAGATGTAG	1799
Db	1777	CATCCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTTGAGATAAGGCTCTCTGCAGATGTAG	1836
Qy	1800	TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTTAAATTCATATGACTGTTTCC	1859
Db	1837	TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTTAAATTCATATGACTGTTTCC	1896
Qy	1860	TTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGGGGGAGACTATGTAAAGATG	1919
Db	1897	TTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGGGGGAGACTATGTAAAGATG	1956
Qy	1920	AAGCAGAGATCGAGTTTTGCGCCACACAGCTAAGAAAAACCAAGGATTTGTGGCAACCA	1979
Db	1957	AAGCAGAGATCGGAGTTTTGCGCCACACAGCTAAGAAAAACCAAGGATTTGTGGCAACCA	2016
Qy	1980	TCAGAAGCTTGGAAAGAGCAAAAGAAATTTCTTCCCTAGAGGCTTTTAGAGGGATAACGGC	2039

Db	2017	TCGAGAGCTTGAAGAGGCGAAGAGAAATCTTCCCTAGAGGCTTTAGAGGATTAACGGC	2076
Qy	2040	TCTGCTGAACCTTAATCTCAGACTTCCAGCTCTCTGAAACGAAGAATAAATTTTCGG	2099
Db	2077	TCTGCTGAACCTTAATCTCAGACTTCCAGCTCTCTGAAACGAAGAATAAATTTTCGG	2136
Qy	2100	CTGTTTTAAGCCACCAAGATAATTTGGTTACAGCAGCTCTAGAAACTTAATACAGTGT	2159
Db	2137	CTGTTTTAAGCCACCAAGATAATTTGGTTACAGCAGCTCTAGAAACTTAATACAGTGT	2196
Qy	2160	AAAATGATCCCTGTCTCTCGTGTTCATCTGTGTGTGTCCTCCACAAATGTACCA	2219
Db	2197	AAAATGATCCCTGTCTCTCGTGTTCATCTGTGTGTGTCCTCCACAAATGTACCA	2256
Qy	2220	AAGTTGTCTTTGTGACCCCAATAGATATGGCAGAAAGTATGGCATGCCACTTCCAAAGATT	2279
Db	2257	AAGTTGTCTTTGTGA-CCAATAGATATGGCAGAAAGTATGGCATGCCACTTCCAAAGATT	2315
Qy	2280	AGTTTATAAAGACACTGAGCTTCTAATTGAGCCCTCTCTCTGCGCACCCACCGCCCC	2339
Db	2316	AGTTTATAAAGACACTGAGCTTCTAATTGAGCCCTCTCTCTGCGCACCCACCGCCCC	2375
Qy	2340	CAATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGTGCCTATGAGCAGGCCTA	2399
Db	2376	CAATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGTGCCTATGAGCAGGCCTA	2435
Qy	2400	TAAAGAGACTTACGTGGTAAATAAAGTCTCTGCGCCACACACATAGTGAACCTA	2459
Db	2436	TAAAGAGACTTACGTGGTAAATAAAGTCTCTGCGCCACACACATAGTGAACCTA	2495
Qy	2460	GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTGTCTCAGTTTTGGTCT	2519
Db	2496	GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTGTCTCAGTTTTGGTCT	2555
Qy	2520	AACTTGTTATGCAAGATAGATAAATAATATATGCAGAGAAAGAG	2562
Db	2556	AACTTGTTATGCAAGATAGATAAATAATATATGCAGAGAAAGAG	2598
RESULT 13			
ACA93772			
ID	ACA93772 standard; cDNA; 2598 BP.		
AC	ACA93772;		
XX			
XX			
DT	17-JUL-2003 (first entry)		
XX			
DE	Human cDNA encoding secreted/transmembrane protein PRO4342.		
XX			
KW	Human; ss; Gene; PRO; secreted protein; transmembrane protein;		
KW	cytostatic; vulnary; osteopathic; antiarthritic; antirheumatic;		
KW	lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;		
KW	liver tumour; tumour necrosis factor; pericyte cell proliferation;		
KW	TNF-alpha; proteoglycans release; cartilage; cancer; wound healing;		
KW	cartilage defect; osteoarthritis; rheumatoid arthritis.		
OS	Homo sapiens.		
XX			
FN	US2003045684-A1.		
XX			
PD	06-MAR-2003.		
XX			
PF	02-MAY-2002; 2002US-00063553.		
XX			
PR	30-DEC-1998; 98KR-00062142.		
PR	08-MAR-1999; 99WO-US005028.		
PR	14-MAY-1999; 99US-00311832.		
PR	14-MAY-1999; 99WO-US010733.		
PR	25-AUG-1999; 99US-00380137.		
PR	25-AUG-1999; 99US-00380138.		
PR	25-AUG-1999; 99US-00380139.		
PR	25-AUG-1999; 99US-00380142.		

PR	15-SEP-1999;	99US-00397342.
PR	18-OCT-1999;	99US-00403297.
PR	12-NOV-1999;	99US-00423844.
PR	30-DEC-1999;	99WO-US031274.
PR	18-FEB-2000;	2000WO-US004341.
PR	01-MAR-2000;	2000WO-US005601.
PR	02-MAR-2000;	2000WO-US005841.
PR	21-MAR-2000;	2000WO-US007532.
PR	22-MAY-2000;	2000WO-US014042.
PR	02-JUN-2000;	2000WO-US015264.
PR	22-AUG-2000;	2000WO-US023328.
PR	24-AUG-2000;	2000US-0064610.
PR	18-SEP-2000;	2000US-00685350.
PR	08-NOV-2000;	2000US-00709238.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032678.
PR	20-DEC-2000;	2000US-00747259.
PR	20-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2001WO-US006520.
PR	22-MAR-2001;	2001US-00816744.
PR	10-MAY-2001;	2001US-00854208.
PR	30-MAY-2001;	2001US-00870574.
PR	01-JUN-2001;	2001WO-US017800.
PR	05-JUN-2001;	2001US-00874503.
PR	29-JUN-2001;	2001US-00869599.
PR	18-JUL-2001;	2001US-00908827.
PR	06-DEC-2001;	2001US-00006867.
XX	(GETH) GENENTECH INC.	
PA	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;	
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;	
XX	WPI: 2003-392892/37.	
DR	P-PSDB; ABU92551.	
XX	New PRO994 polypeptide, useful for detecting tumors, or for stimulating	
PT	Tumor Necrosis Factor alpha, or pericyte proliferation, especially for	
PT	treating cancer, cartilage defects, osteoarthritis and rheumatoid	
PT	arthritis in a mammal.	
XX	Disclosure; Fig 151; 235pp; English.	
PS	The invention relates to a new isolated PRO994 polypeptide comprises an	
CC	amino acid sequence appearing as ABU92499, PRO994 lacking its associated	
CC	signal peptide, the extracellular domain of PRO994, the extracellular	
CC	domain of PRO994 (lacking it associated signal peptide) or the protein	
CC	encoded by the full-length coding sequence of the cDNA ATCC 203018. Also	
CC	included is a chimaeric molecule comprising the PRO994 polypeptide fused	
CC	to a heterologous amino acid sequence. The PRO polypeptide is useful in	
CC	pharmaceuticals, diagnostics, biosensors or bioreactors. It is	
CC	particularly useful for detecting tumors (e.g. lung tumour, colon	
CC	tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)	
CC	in a mammal, for stimulating the release of tumour necrosis factor (TNF)-	
CC	alpha from human blood, for stimulating the proliferation of pericyte	
CC	cells, or stimulating the release of proteoglycans from cartilage. The	
CC	polypeptide may be employed for a variety of therapeutic purposes, e.g.	
CC	for treating cancer, wound healing, cartilage defects, osteoarthritis,	
CC	rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83	
CC	other PRO polypeptides and their encoding cDNAs. The present sequence	
CC	encodes a PRO polypeptide of the invention	
XX	Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;	
SQ	Query Match 98.1%; Score 2514.2; DB 8; Length 2598;	
		Best Local Similarity 99.6%; Pred. No. 0;
		Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
Qy	1 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGCTCCGAA 60	
Db	38 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGCTCCGAA 97	

QY 61 TGAAGACTCGGCAATGAAGGTGCTTTATCTGCAATAAACAGCTTCTAGCTGGAGGC 120
Db 98 TGAAGACTCGGCAATGAAGGTGCTTTATCTGCATAATAACAGCTTCTAGCTGGAGGC 157
QY 121 TGCATGACGGGAAGTCAATAAGGTGAAGAGATCAGCGTGTCCCAATCGGTGGCTGG 180
Db 158 TGCATGACGGGAAGTCAATAAGGTGAAGAGATCAGCGTGTCCCAATCGGTGGCTGG 217
QY 181 ATGCCAGCTGTCCCGGTCATCTCGGTGTCCAGGTGGAAGCCAGTGCCTGTGATGTG 240
Db 218 ATGCCAGCTGTCCCGGTCATCTCGGTGTCCAGGTGGAAGCCAGTGCCTGTGATGTG 277
QY 241 GGGTGGGAGGAGCCGACTCTAAACATAGAGCCAGTGAACATCATGAGGCTCTATCTTG 300
Db 278 GGGTGGGAGGAGCCGACTCTAAACATAGAGCCAGTGAACATCATGAGGCTCTATCTTG 337
QY 301 GTGCCAAGGAATCCAAGAGCTTCACTTCTACGGGGGAGACATGGGGCTCACTCGAGCT 360
Db 338 GTGCCAAGGAATCCAAGAGCTTCACTTCTACGGGGGAGACATGGGGCTCACTCGAGCT 397
QY 361 TCGAGTGGGCTGCCCTACCCGGCTGGTTCCTGTGCACGGTGTCTGAAGCCGATCAGCCTG 420
Db 398 TCGAGTGGGCTGCCCTACCCGGCTGGTTCCTGTGCACGGTGTCTGAAGCCGATCAGCCTG 457
QY 421 TCAGACTCACCCAGCTTCCCGAGAATGGTGGTGGAAATGCCCCATCAAGACTTCTACT 480
Db 458 TCAGACTCACCCAGCTTCCCGAGAATGGTGGTGGAAATGCCCCATCAAGACTTCTACT 517
QY 481 TCCAGAGTGTACATAGGCAAGTGTCCCGCCAGAACTCCCTGGGAGAGCCAGCTGG 540
Db 518 TCCAGAGTGTACATAGGCAAGTGTCCCGCCAGAACTCCCTGGGAGAGCCAGCTGG 576
QY 541 GTGAGGGGTGAGTGAGGAGAGCCATGGCGGCAATCACTTCTTCTGCTCTCAGGACCC 600
Db 577 GTGAGGGGTGAGTGAGGAGAGCCATGGCGGCAATCACTTCTTCTGCTCTCAGGACCC 636
QY 601 CAGGTCTGACTAGTGGGCACTGACACTTGTCTTCTGTGTTCCAGTTTCATAAAT 660
Db 637 CAGGTCTGACTAGTGGGCACTGACACTTGTCTTCTGTGTTCCAGTTTCATAAAT 696
QY 661 CTGAGATTGGAGCTCAGTCCAGGTCTCCCGCACTGGATGGTGTCTGTGGAGC 720
Db 697 CTGAGATTGGAGCTCAGTCCAGGTCTCCCGCACTGGATGGTGTCTGTGGAGC 756
QY 721 CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAAAGATTTCTGTGGGGTGG 780
Db 757 CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAAAGATTTCTGTGGGGTGG 816
QY 781 GTGGGGAGTGTGGGAATCATTCCTGTCTTAATGTGAACAGTGTACCTGAGCC 840
Db 817 GTGGGGAGTGTGGGAATCATTCCTGTCTTAATGTGAACAGTGTACCTGAGCC 876
QY 841 CCGGAGGCCAACCCATCCCGAGTGGCTTATAGGTCAGTAGCTCTCCACATGAAGTC 900
Db 877 CCGGAGGCCAACCCATCCCGAGTGGCTTATAGGTCAGTAGCTCTCCACATGAAGTC 936
QY 901 CTCTCACTCACCACCTGTGCAGAGAGGAGGTGTCTATAGAGTCAGGGATCTATGSCCT 960
Db 937 CTGTCACTCACCACCTGTGCAGAGAGGAGGTGTCTATAGAGTCAGGGATCTATGSCCT 996
QY 961 TGGCCCGAGCCCAACCCCTTCCCTTT-ATCCTGCCATGTGCATATGCTACCTTTCTATC 1019
Db 997 TGGCCCGAGCCCAACCCCTTCCCTTTAATCCTGCCACTGTCTATGCTACCTTTCTATC 1056
QY 1020 TCTTCCTCATCATCTTGTGTGGGATCAGAGGTGGTGTGATGTCAAGAAATGGTTGG 1079
Db 1057 TCTTCCTCATCATCTTGTGTGGGATCAGAGGTGGTGTGATGTCAAGAAATGGCTCG 1116
QY 1080 AGCTCAGAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAACCCAAAGATACA 1139
Db 1117 AGCTCAGAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAACCCAAAGATACA 1176

QY 1140 ATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAGTCTCATGACATATTGAGAA 1199
Db 1177 ATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAGTCTCATGACATATTGAGAA 1236
QY 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTAAATTAAGATACCTATTATA 1259
Db 1237 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTAAATTAAGATACCTATTATA 1296
QY 1260 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAAGGTG 1319
Db 1297 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAAGGTG 1356
QY 1320 TGGCAGTATAGGTGATTTTCTTTTAAATCTCTTAAATTTATCTGTATTCTTAAATTTTC 1379
Db 1357 TGGCAGTATAGGTGATTTTCTTTTAAATCTCTTAAATTTATCTGTATTCTTAAATTTTC 1416
QY 1380 TACAATGAAGATGAATTCCTGTATAAAAATAAGAAAAAGAAATTAATCTTGAAGTAAGCA 1439
Db 1417 TACAATGAAGATGAATTCCTGTATAAAAATAAGAAAAAGAAATTAATCTTGAAGTAAGCA 1476
QY 1440 GAGCAGACATCATCTCTGATTTCTCTCAGCTTCCCAATTTCCCGAGAGTAAATTCAAATTGA 1499
Db 1477 GAGCAGACATCATCTCTGATTTCTCTCAGCTTCCCAATTTCCCGAGAGTAAATTCAAATTGA 1536
QY 1500 ATCGAGCTCTGCTGCTCTGGTGTGTAGTGTATCAGGAAACAGATCTCAGCAAGC 1559
Db 1537 ATCGAGCTCTGCTGCTCTGGTGTGTAGTGTATCAGGAAACAGATCTCAGCAAGC 1596
QY 1560 CACTCAGAGGAGGCTGTCTGAGTTGTGGCTGGAAATCTCTGGTAAGGAATCTTAA 1619
Db 1597 CACTCAGAGGAGGCTGTCTGAGTTGTGGCTGGAAATCTCTGGTAAGGAATCTTAA 1656
QY 1620 GAAACAAAATCATCTGTGTAATTTCTTCTAGAGGATCACAGCCCTCTGGATTCAGAGC 1679
Db 1657 GAAACAAAATCATCTGTGTAATTTCTTCTAGAGGATCACAGCCCTCTGGATTCAGAGC 1716
QY 1680 ATTGATCAGTCTCTAAGAGGCTGTCTAGTGTGAAATTTGTGTCCTCCCTCAAAATCA 1739
Db 1717 ATTGATCAGTCTCTAAGAGGCTGTCTAGTGTGAAATTTGTGTCCTCCCTCAAAATCA 1776
QY 1740 CATCTCTCTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGAGATGTAG 1799
Db 1777 CATCTCTCTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGAGATGTAG 1836
QY 1800 TTAGTTAAGACAAGGTCTAGTGTGAGTGAAGTGAACCTTAAATTTCAATATGACTGTTCC 1859
Db 1837 TTAGTTAAGACAAGGTCTAGTGTGAGTGAAGTGAACCTTAAATTTCAATATGACTGTTCC 1896
QY 1860 TTGTATGAAAAGGAGAGACACAGACACAGAGGACGCGGGGAGACTATGTAAAGATG 1919
Db 1897 TTGTATGAAAAGGAGAGACACAGACACAGAGGACGCGGGGAGACTATGTAAAGATG 1956
QY 1920 AAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTTGGCAACA 1979
Db 1957 AAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTTGGCAACA 2016
QY 1980 TCAGAGCTTGAAGAGGCAAGAAATTTCTTCTAGAGGCTTTTAGAGGATTAACGCGC 2039
Db 2017 TCAGAGCTTGAAGAGGCAAGAAATTTCTTCTAGAGGCTTTTAGAGGATTAACGCGC 2076
QY 2040 TCTGCTGAAAACCTTAAATCTCAGACTTCCAGCTCTCTGAACGAAGAAAGATTAATTTCCG 2099
Db 2077 TCTGCTGAAAACCTTAAATCTCAGACTTCCAGCTCTCTGAACGAAGAAAGATTAATTTCCG 2136
QY 2100 CTGTTTTTAAGCCACCAAGGATAATTTGGTTTACAGAGCTCTAGGAACTAATACAGTGTCT 2159
Db 2137 CTGTTTTTAAGCCACCAAGGATAATTTGGTTTACAGAGCTCTAGGAACTAATACAGTGTCT 2196
QY 2160 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCCTCCCTCCCAATGTACCA 2219
Db 2197 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCCTCCCTCCCAATGTACCA 2256
QY 2220 AAGTTGTCTTTGTGACCCCAATAGATATGCGAGAGTGTGCGATGCCACTTCCAGATT 2279

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Db 2257 AAGTTGCTTTTGA-CCATAGAAATATGCGAGAGTATGCGATGCCACTTCCAAAT 2315
Qy 2280 AGTTTATAAAGACACTGACGCTTCTACTTTGAGCCCTCTCTCTGCCACCCACCGCCCC 2339
Db 2316 AGTTTATAAAGACACTGACGCTTCTACTTTGAGCCCTCTCTCTGCCACCCACCGCCCC 2375
Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGGAGCCCTA 2399
Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGGAGCCCTA 2435
Qy 2400 TAAAGAGACTTACGTGTTAAATAAAGTCTCTGCCACACGACATTAAGTGAACCTA 2459
Db 2436 TAAAGAGACTTACGTGTTAAATAAAGTCTCTGCCACACGACATTAAGTGAACCTA 2495
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555
Qy 2520 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562
Db 2556 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2598
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RESULT 14

ACA67346
ID ACA67346 standard; cDNA; 2598 BP.

AC ACA67346;

DT 23-JUN-2003. (first entry)

DE cDNA encoding human secreted polypeptide PRO4342.

KW Human; gene; ss; affinity purification.

OS Homo sapiens.

PN US2003027212-A1.

PD 06-FEB-2003.

PF 02-MAY-2002; 2002US-00063544.

PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.

PR 15-SEP-1999; 99US-00397342.

PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.

PR 30-DEC-1999; 99WO-US031274.

PR 18-FEB-2000; 2000WO-US004341.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 21-MAR-2000; 2000WO-US007532.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00654610.

PR 18-SEP-2000; 2000US-00665350.

PR 08-NOV-2000; 2000US-00709238.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 22-MAR-2001; 2001US-00816744.

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PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00068667.
XX (GETH ) GENENTECH INC.
XX
PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX P-PSDB; ABU81221.
DR WPI; 2003-341840/32.
XX P-PSDB; ABU81221.
XX
PT New monoclonal antibody that binds to a secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and also
PT for treating conditions responsive to the antibody.
XX
PS Example 4; Fig 151; 235pp; English.
XX
CC The invention relates to an antibody that binds to a secreted and
CC transmembrane polypeptide, PRO1136. The antibody is useful for preparing
CC a medicament useful in the treatment of a condition responsive to anti-
CC PRO antibody. The antibody is also useful in diagnostic assays for PRO,
CC by detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence represents a cDNA encoding a PRO
CC polypeptide of the invention
XX
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
Query Match 98.1%; Score 2514.2; DB 8; Length 2598;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
Qy 1 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGTTCCGAA 60
Db 38 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGTTCCGAA 97
Qy 61 TGAAGGACTCGGCATTTGAAGTGTCTTATCTGCAATAATAACAGCTTTAGCTGGAGGC 120
Db 98 TGAAGGACTCGGCATTTGAAGTGTCTTATCTGCAATAATAACAGCTTTAGCTGGAGGC 157
Qy 121 TGCATGCGAGGAGGCTCATTAAAGTGAAGATCAGCGTGTCCCAATCGTGCTCG 180
Db 158 TGCATGCGAGGAGGCTCATTAAAGTGAAGATCAGCGTGTCCCAATCGTGCTCG 217
Qy 181 ATGCCAGCTGTCCCGGCTCATCTCTGGGTGTCCAGGTGGAAGCCAGTGCCTGTCTATGTG 240
Db 218 ATGCCAGCTGTCCCGGCTCATCTCTGGGTGTCCAGGTGGAAGCCAGTGCCTGTCTATGTG 277
Qy 241 GGGTGGGCGAGGAGCGACTCTTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
Db 278 GGGTGGGCGAGGAGCGACTCTTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337
Qy 301 GTGCCAAGGAATCCAAAGCTTTCACCTTCCCGGGGAGACATGGGGCTCACCTCCAGCT 360
Db 338 GTGCCAAGGAATCCAAAGCTTTCACCTTCCCGGGGAGACATGGGGCTCACCTCCAGCT 397
Qy 361 TCGAGTTCGGCTTACCGGGCTGTCTCTGTCACGCGTGTCTGAAGCCGATCAGCCTG 420
Db 398 TCGAGTTCGGCTTACCGGGCTGTCTCTGTCACGCGTGTCTGAAGCCGATCAGCCTG 457
Qy 421 TCAGACTCACCCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCCATTCAGACTTCTACT 480
Db 458 TCAGACTCACCCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCCATTCAGACTTCTACT 517
Qy 481 TCCAGCAGTGTACTTAGGGCAACGTGCCCGCCCGCAAACTCCCTGGGCGAGCAGCTCGG 540
Db 518 TCCAGCAGTGTACTTAGGGCAACGTGCCCGCCCGCAAACTCCCTGGGCGAGCAGCTCGG 576
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QY	541	GTGAGGGT	GAGTGGAGGAGACCATGGCGACAATCACTCTTTCTGCTCTCAGGACCCC	600
DB	577	GTGAGGGT	GAGTGGAGGAGACCCATGGCGACAATCACTCTCTCTGCTCTCAGGACCCC	636
QY	601	CAGGTC	GACTTAGTGGGCACTGACCACTTTGTCTTCGTGTTCCCAAGTTTGATAAATT	660
DB	637	CAGGTC	GACTTAGTGGGCACTGACCACTTTGTCTTCGTGTTCCCAAGTTTGATAAATT	696
QY	661	CTGAGATT	TGGAGCTCAGTCCAGGGTCCTCCCCACATGGATGGTGTCTACTGCTGTGGAAC	720
DB	697	CTGAGATT	TGGAGCTCAGTCCA CGGTCTCTCCCCACATGGATGGTGTCTACTGCTGTGGAAC	756
QY	721	CTTGTA	AAAAACCATGTGGGTAAACCTGGGAATAACATGAAAGAAATTTCTGTGGGGTGGG	780
DB	757	CTTGTA	AAAAACCATGTGGGTAAACCTGGGAATAACATGAAAGAAATTTCTGTGGGGTGGG	816
QY	781	GTGGGG	AGTGTGGGAATCATTTCTGCTTAATGGTAACTGCAAGGTGTTACCTCTGAGCC	840
DB	817	GTGGGG	AGTGTGGGAATCATTTCTGCTTAATGGTAACTGCAAGGTGTTACCTCTGAGCC	876
QY	841	CCGAGG	CCAAACCATCCCAAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC	900
DB	877	CCGAGG	CCAAACCATCCCAAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC	936
QY	901	CTCTCA	CTCACTCACTGTGCAAGGAGGAGGTGGTCATAGAGTCAGGGATCTATGCGCCCT	960
DB	937	CTGTCA	CTCACTCACTGTGCAAGGAGGAGGTGGTCATAGAGTCAGGGATCTATGCGCCCT	996
QY	961	TGGCCG	AGCCCCACCCCTTCCCTTTT-ATCCTGCGCACTGTCATATGCTACTCTTCTCTATC	1019
DB	997	TGGCCG	AGCCCCACCCCTTCCCTTTTAACTCTGCGCACTGTCATATGCTACTCTTCTCTATC	1056
QY	1020	TCCTTC	CCCTCATCATCTTTGTTGTGGGCATAGGAGGTGGTGTATGTCAGAGAAATGTTTCG	1079
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QY	1140	ATCAAA	ATCCAGATGCTGGTCTCTATTCCCATGAAAAGTGTCTATGACATATTGAGAA	1199
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QY	1200	GACCTAC	TTCACAAAGTGGCATATATTCGAATTTATTTTAAATAAAGATACCTATTATTA	1259
DB	1237	GACCTAC	TTCACAAAGTGGCATATATTCGAATTTATTTTAAATAAAGATACCTATTATTA	1296
QY	1260	TATTTCT	TATTAGAAAAAGCTCGAGAGTTTACTTCAATTTGTAGCAATGTGAGGGTGG	1319
DB	1297	TATTTCT	TATTAGAAAAAGCTCGAGAGTTTACTTCAATTTGTAGCAATGTGAGGGTGG	1356
QY	1320	TGGCAG	TATAGTGCATTTTCTTTTAACTCTGTTAAATTTATTTCTGTATTTCTTAATTTTTC	1379
DB	1357	TGGCAG	TATAGTGCATTTTCTTTTAACTCTGTTAAATTTATTTCTGTATTTCTTAATTTTTC	1416
QY	1380	TACAAT	GAAGATGAATTCCTTGTAATAAAAAATAAGAAAAAGAAATTAATCTTTGAGGTAAAGCA	1439
DB	1417	TACAAT	GAAGATGAATTCCTTGTAATAAAAAATAAGAAAAAGAAATTAATCTTTGAGGTAAAGCA	1476
QY	1440	GAGCAG	ACATCATCTCTGATTGTCTCTCAGCCTCCAATTTCCCGAGAGTAAATTCAAATTGA	1499
DB	1477	GAGCAG	ACATCATCTCTGATTGTCTCTCAGCCTCCAATTTCCCGAGAGTAAATTCAAATTGA	1536
QY	1500	ATCCAG	CTCTGCTCTGGTTGGTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAAGC	1559
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QY	1560	CACTGA	GAGGAGCTGTGCTGAGTTTGTGTGGCTGGAAATCTCTGGGTAAAGGAATTTAAA	1619
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RESULT 15
ACH66319
ID ACH6
XX
AC ACH6
XX
DT 14-O
XX

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Db		
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QY		
1717	ATTGGATCCAGTCTCTAAGAAGCTCGTACTGTTGTAATTGTGTGCCCTCAAATTCA	1776
Db		
1740	CATCCTCTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGCTCTCTGCAGATGTAG	1799
QY		
1777	CATCCTCTTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGCTCTCTGCAGATGTAG	1836
Db		
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QY		
1837	TTAGTTAAGACAAGTCACTGCTGGATGAAGGTAGACTTAAATTCAATATGACTGGTTTCC	1896
Db		
1860	TTGTATGAAGAAGAGGACACAGACACAGAGAGACGCGGGAAGACTATGTAAAGATG	1919
QY		
1897	TTGTATGAAGAAGAGGACACAGACACAGAGAGACGCGGGAAGACTATGTAAAGATG	1956
Db		
1920	AAGCAGAGATCGAGTGTTCAGCCACACAGCTTAAGAAACACCAAGGATTTGTGGCAACCA	1979
QY		
1957	AAGCAGAGATCGAGTGTTCAGCCACACAGCTTAAGAAACACCAAGGATTTGTGGCAACCA	2016
Db		
1980	TCAGAAGCTTGAAGAGGCAAGAAGAAATTCCTCCCTAGAGGCTTTAGAGGATTAACGGC	2039
QY		
2017	TCAGAAGCTTGAAGAGGCAAGAAGAAATTCCTCCCTAGAGGCTTTAGAGGATTAACGGC	2076
Db		
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QY		
2077	TCCTGCTGAAACCTTAATCTCAGACTTCAGGCTCCCTGAACGAAGAAGATAAATTCGG	2136
Db		
2100	CTGTGTTTAAGCCACCAAGGATAATTTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCT	2159
QY		
2137	CTGTGTTTAAGCCACCAAGGATAATTTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCT	2196
Db		
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QY		
2197	AAATGATCCCTGTCTCTCGTGTTTACATTCGTGTGTGTCTCCCTCCCAATGTACCA	2256
Db		
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QY		
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Db		
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QY		
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Db		

RESULT 15
ACH66319
ID ACH66319 standard; cDNA; 2598 BP
XX
XX
AC ACH66319;
XX
DT 14-OCT-2003 (first entry)
XX

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:56:15 ; Search time 8384.03 Seconds
(without alignments)
11636.250 Million cell updates/sec

Title: US-09-617-720A-1

Perfect score: 2563

Sequence: 1 aggggagctacacctgtg.....ataatgcagagaagaaga 2563

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2469.2	96.3	2605	3	CR613851 full-length
2	1568.4	61.2	1648	3	BC000945 Homo sapi
3	980.2	38.2	1140	1	AL570964 AL570964
4	731.6	28.5	1080	7	CK232552 ILLUMIGEN
5	712.6	27.8	985	1	AL545100 AL545100
6	707.7	27.6	750	5	EX091500 EX091500
7	683.8	26.7	726	4	BI089828 602855071
8	656.2	25.6	876	5	EX350082 EX350082
9	644.6	25.2	702	6	CA310393 UI-H-FT1-
10	643.2	25.1	697	2	BF509095 UI-H-B14-
11	631.6	24.6	858	4	BI090567 602855674
12	551.4	21.5	915	5	EX350083 EX350083
13	527.8	20.6	555	1	AU138695 AU138695
14	481	18.8	555	5	BQ351235 RCO-HT077
15	468	18.3	468	9	AY413262 Homo sapi
16	467	18.2	632	7	CV029389 8151 Full
17	465	18.1	467	8	AZ521126 RFI-11-1
18	463.2	18.1	468	9	AY413263 Pan trogl
19	451.2	17.6	485	1	AI040890 ow26a12.x
20	436.8	17.0	464	2	BF435174 nab43h02.
21	427.8	16.7	464	1	AI831402 wj64a07.x
22	418	16.3	442	1	AI469873 tJ88a08.x
23	398.2	15.5	414	1	AA722902 sg81a03.s
24	393.6	15.4	435	2	BE711845 QV2-HT069

C	25	387.4	15.1	410	1	AI167887	0291C09.x
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	27	384.6	15.0	1199	3	AK008977	Mus muscu
C	28	380.8	14.9	416	1	AUI57708	AUI57708
	29	379.8	14.8	862	6	CB590160	AGENCOURT
	30	379.4	14.8	2841	3	AK014576	Mus muscu
	31	373.4	14.6	885	6	CB589411	AGENCOURT
	32	367	14.3	414	7	CR742272	CR742272
	33	366.6	14.3	1531	3	AK010020	Mus muscu
	34	360	14.0	708	6	BY709379	BY709379
	35	349.6	13.6	400	4	BG010066	PM4-GN030
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	37	327	12.8	439	9	AY413264	Mus muscu
	38	315.4	12.3	348	7	R70089	Y148G04.r1
	39	300	11.7	338	5	BX477358	DKF2p6860
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	41	263	10.3	691	6	BY754693	BY754693
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ALIGNMENTS

RESULT 1	CR613851	2605 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CSOD1013YA07 of Placent	Cot 25-normalized			
DEFINITION	of Homo sapiens (human).				
ACCESSION	CR613851				
VERSION	CR613851.1	GI:50494658			
KEYWORDS	HTC; CNSLT CDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2605)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600				

QY 61 TGAAGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACAGCTTCTAGCTGGAGGC 120
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QY 421 TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTTGGAAATGCCCCATCACAGACTTCTACT 480
Db 494 TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTTGGAAATGCCCCATCACAGACTTCTACT 553
QY 481 TCCAGCAGTGTGACTAGGGCAACGTGCCCGCCCGAGAACTCCCTGGGCGAGCCAGCTCGG 540
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QY 541 GTGAGGGTGAAGTGGAGAGACCCATGGCGGCAATCACTTCTGCTCTCAGGACCCC 600
Db 613 GTGAGGGTGAAGTGGAGAGACCCATGGCGGCAATCACTTCTGCTCTCAGGACCCC 672
QY 601 CAGGCTGACTTAGTGGGCACTGACACTTGTCTTCTGCTTCCAGATTTGCATAAAT 660
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RESULT 2
BC000945
LOCUS
DEFINITION
Homo sapiens interleukin 1 family, member 5 (delta), mRNA (cDNA
clone IMAGE:3447369), with apparent retained intron.
ACCESSION
BC000945
VERSION
BC000945.2
KEYWORDS
SOURCE
GI:14705316
ORGANISM
Homo sapiens (human)

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REFERENCE
AUTHORS
Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.W., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalley,D.B.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2238257
MEDLINE
PUBMED
12477932
2 (bases 1 to 1648)
Strausberg,R.
Direct Submission
Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
On Jul 12, 2001 this sequence version replaced gi:13937574.
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.

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FEATURES
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/note="Vector: pCMV-SPORT6"

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 3 Row: i Column: 18
This clone has the following problem: retained intron.
Location/Qualifiers

```

```

ORIGIN
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Best Local Similarity 99.2%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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QY 1014 CTTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGTCATCTCAGAGAAAT 1073
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QY 1134 GATACAATCAAAATCCAGATGCTGCTCTCTATTTCCATGAAAAAGTGTCTCATGACATAT 1193
DB 181 GATACAATCAAAATCCAGATGCTGCTCTCTATTTCCATGAAAAAGTGTCTCATGACATAT 240

QY 1194 TGAGAGAGACCTACTTACAAAGTGGCATATATTCGAATTTTAAATTAAGAGATACCTA 1253
DB 241 TGAGAGAGACCTACTTACAAAGTGGCATATATTCGAATTTTAAATTAAGAGATACCTA 300

QY 1254 TTTATATATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTTCAATTGTAGCAATGTCA 1313
DB 301 TTTTATTTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTTCAATTGTAGCAATGTCA 360

QY 1314 GGGTGGTGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAA 1373
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QY 1374 TTTTCTACATGAAGATGAATTCCTCTATATAAATAAGAAAGAAATTAATCTTGAGG 1433
DB 421 TTTTCTACATGAAGATGAATTCCTCTATATAAATAAGAAAGAAATTAATCTTGAGG 480

QY 1434 TAAAGCAGACACATCATCTCTGATTTGCTCAGCCTCCAATTCGCCAGAGTAAATTTCA 1493
DB 481 TAAAGCAGACACATCATCTCTGATTTGCTCAGCCTCCAATTCGCCAGAGTAAATTTCA 540

QY 1494 AATTGAATCGAGCTCTGCTGCTCTGTTGGTTGTTAGTAGTATCAGGAAACAGATCTCAG 1553
DB 541 AATTGAATCGAGCTCTGCTGCTCTGTTGGTTGTTAGTAGTATCAGGAAACAGATCTCAG 600

QY 1554 CAAAGCCACTGAGGAGGAGGCTGCTGATGTTGTGCTGGAATCTCTGGTGAAGNA 1613
DB 601 CAAAGCCACTGAGGAGGAGGCTGCTGATGTTGTGCTGGAATCTCTGGTGAAGNA 660

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

```

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QY 1614 CTTAAAGAACAAATCATCTGGTAATCTTCTTCTAGAGGATCAGCCCTGGGATTC 1673
Db 661 CTTAAAGAACAAATCATCTGGTAATCTTCTTCTAGAGGATCAGCCCTGGGATTC 720
QY 1674 CAAGGCATTTGGATCCAGTCTCTAAGAGGCTCTGTACTGTGGTGAATTTGTGCCCCCTCA 1733
Db 721 CAAGGCATTTGGATCCAGTCTCTAAGAGGCTCTGTACTGTGGTGAATTTGTGCCCCCTCA 780
QY 1734 AATTACATCTCTTTGGAAATCTAGTCGTGAGTATTTTGGAGATAAGTCTCTGAG 1793
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QY 1854 GTTTCCTCTGTATGAAAGGAGAGGACACAGAGACAGAGGAGCGGGGAAAGACTATGTA 1913
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QY 1914 AAGATGAAGCAGAGATTCGAGTTTTCGAGCCACAGCTAAGAAACACCAAGATTTGG 1973
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QY 1974 CAACCATCAGAGCTTTGGAAGGCAAGAAAGAAATTTCTTCCCTAGAGGCTTTAGAGGGAT 2033
Db 1021 CAACCATCAGAGCTTTGGAAGGCAAGAAAGAAATTTCTTCCCTAGAGGCTTTAGAGGGAT 1080
QY 2034 AACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAGCCTCTGAAAGAAAGAAATAAA 2093
Db 1081 AACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAGCCTCTGAAAGAAAGAAATAAA 1140
QY 2094 TTTCCGGCTGTTTAAAGCCCAAGGATAATTTGTTACAGAGCTCTAGAAACTAATACA 2153
Db 1141 TTTCCGGCTGTTTAAAGCCCAAGGATAATTTGTTACAGAGCTCTAGAAACTAATACA 1200
QY 2154 GCTGCTAAATGATCCCTGCTCTCTGTTGTTTACATTTCTGTGTGTCCTTCCCTCCCAAT 2213
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QY 2274 AAGATTAGTTATAAAGACACTGCAGCTTCTACTTGGCCCTCTCTCTGCCCCAC 2333
Db 1320 AAGATTAGTTATAAAGACACTGCAGCTTCTACTTGGCCCTCTCTCTGCCCCAC 1379
QY 2334 CGCCCCCAATCTATTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCAATGCTATGACA 2393
Db 1380 CGCCCCCAATCTATTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCAATGCTATGACA 1439
QY 2394 GGCCTATAAAGAGACTTACGTGTAATAAATAGAGTCTCTGCCCCACAGCCACATTAGTG 2453
Db 1440 GGCCTATAAAGAGACTTACGTGTAATAAATAGAGTCTCTGCCCCACAGCCACATTAGTG 1499
QY 2454 AACCTAGAGCAGAGACTCTGTGAGATAATCGATTTGTTGTTTAAAGTTGCTCAGTTT 2513
Db 1500 AACCTAGAGCAGAGACTCTGTGAGATAATCGATTTGTTGTTTAAAGTTGCTCAGTTT 1559
QY 2514 TGGTCTAACTTGTATGAGCAATAGATAAATATATATGAGAAAGAGA 2563
Db 1560 TGGTCTAACTTGTATGAGCAATAGATAAATATATATGAGAAAGAGA 1609

RESULT 3
AL570964/c 1140 bp mRNA linear EST 05-APR-2004
LOCUS AL570964 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1013YA07 3-PRIME, mRNA sequence.
ACCESSION AL570964
VERSION AL570964.3 GI:46237085
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EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1140)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31292372.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1383.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1013AA04NP1&c=1383.f.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1013YA07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 38.2%; Score 980.2; DB 1; Length 1140;
Best Local Similarity 98.9%; Pred. No. 3.2e-242; Indels 2; Gaps 2;
Matches 1004; Conservative 3; Mismatches 6;

QY 1519 GTTGGTTGTAGTAGATCAGGAACAGATCTCAGAAAGCCACTGAGGAGGCTGTG 1578
Db 1013 GXTKGTGTGTAGTAGATCA-GAAACAGATCTCAGAAAGCCACTGAGGAGGCTGTG 955
QY 1579 CTGAGTTTGTGTGGTGAATCTCTGGGTAGGAATCTTAAAGAACAAAATCATCTGTA 1638
Db 954 ATGAGTTTGTGTGGTGAATCTCTGGGTAGGAATCTTAAAGAACAAAATCATCTGTA 895
QY 1639 ATTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGATTCAGATCTCTTAAG 1698
Db 894 ATTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGATTCAGATCTCTTAAG 835
QY 1699 AAGGCTGTGTACTGTTGAATTTGTGTCCTCCCTCAAAATTCACATCTTCTTGAATCTCA 1758
Db 834 AAGGCTGTGTACTGTTGAATTTGTGTCCTCCCTCAAAATTCACATCTTCTTGAATCTCA 775
QY 1759 GTCTGTGATTTATTGGAGATAAGGCTCTCCAGATGTAGTTAGTAAAGAGGTCAT 1818
Db 774 GTCTGTGATTTATTGGAGATAAGGCTCTCCAGATGTAGTTAGTAAAGAGGTCAT 715
QY 1819 GCTGGATGAAGGTAGACCTAAATTTCAATATGACTGGTTTCTTGTATGAAAAGGAGAGA 1878
Db 714 GCTGGATGAAGGTAGACCTAAATTTCAATATGACTGGTTTCTTGTATGAAAAGGAGAGA 655
QY 1879 CACAGAGACAGAGGAGACCGGGGAGACTATGTAAAGATGAAGGACAGATCGGAGTTT 1938
Db 654 CACAGAGACAGAGGAGACCGGGGAGACTATGTAAAGATGAAGGACAGATCGGAGTTT 595
QY 1939 TGCAGCCACAGCTAAGAAACACCAAGGATTTGGCAACCATCAGAGCTTCGAAAGAGGC 1998
Db 594 TGCAGCCACAGCTAAGAAACACCAAGGATTTGGCAACCATCAGAGCTTCGAAAGAGGC 535
QY 1999 AAAGAAGAATTTCTTCCCTAGAGGCTTTAGAGGGGATAACGGCTCTGCTGAAACCTTAATCT 2058

KEYWORDS
SOURCE ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

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|||||
Db 534 AAAGAGAATCTTCCCTAGAGCTTTAGAGGATAACGGCTCTGCTGAACCTTAATCT 475
QY 2059 CAGACTTCAGGCTCTCTGAACGAAGAAATAAATTTTCGGCTGTTTAAAGCCACCAAGG 2118
Db 474 CAGACTTCAGGCTCTCTGAACGAAGAAATAAATTTTCGGCTGTTTAAAGCCACCAAGG 415
QY 2119 ATAATTTGGTTACAGAGCTCTAGGAACTAATAACAGCTGCTAAATGATCCCTGCTCT 2178
Db 414 ATAATTTGGTTATGGCAGCTCTAGGAACTAATAACAGCTGCTAAATGATCCCTGCTCT 355
QY 2179 CGTGTTCATCTGTGTGTGTCCTCCCAACATGTACCAAGTTGCTTTGTGACCA 2238
Db 354 CGTGTTCATCTGTGTGTGTCCTCCCAACATGTACCAAGTTGCTTTGTGGA-CCA 296
QY 2239 ATAGAATATGGCAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2298
Db 295 ATAGAATATGGCAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 236
QY 2299 AGCTTCTACTGAGCCCTCTCTCTGCAACCCACCCGCCCCCAATCTATCTTGGCTCACT 2358
Db 235 AGCTTCTACTGAGCCCTCTCTCTGCAACCCACCCGCCCCCAATCTATCTTGGCTCACT 176
QY 2359 CGCTCTGGGGAGCTAGCTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 2418
Db 175 CGCTCTGGGGAGCTAGCTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 116
QY 2419 AAAATGAAGTCTCTGCCCCACAGCCACATTTAGTGAACCTTAGAAGCAGAGACTCTGTG 2478
Db 115 AAAATGAAGTCTCTGCCCCACAGCCACATTTAGTGAACCTTAGAAGCAGAGACTCTGTG 56
QY 2479 ATAATCGATGTTGTTGTTTAAAGTTGCTCAGTTTGGTCTAACTTGTGTTATGCGAG 2533
Db 55 ATAATCAATGTTGTTGTTTAAAGTTGCTCAGTTTGGTCTAACTTGTGTTATGCGAG 1
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RESULT 4

CK232552
LOCUS
DEFINITION ILLUMIGEN_MCO_4234 Katze MMP2 Macaca mulatta cDNA 5' similar to human IL1F5 (Hs.207224), mRNA sequence.

ACCESSION CK232552

VERSION CK232552.1 GI:39638910

KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM

Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

REFERENCE 1 (bases 1 to 1080)

AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

TITLE Large-scale Rhesus Macaque cDNA Sequencing

JOURNAL Unpublished (2003)

COMMENT Contact: C. Magness

ILLUMIGEN Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2003.12.02. 777 Q20 bases. Assembles in contig w/ 1

member(s). Contig contains 1 (0%) lib members.

PCR PRIMERS

FORWARD: CCCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGGCGAATTGGTA

Insert Length: 1080 Std Error: 0.00

Place: CL000050 row: B column: 10

Seq primer: CCCTCACTAAAGGGAACAAA

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..1080

/organism="Macaca mulatta"

/mol_type="mRNA"

/strain="Indian"

Query Match 28.5%; Score 731.6; DB 7; Length 1080;
Best Local Similarity 89.6%; Pred. No. 7.8e-178;
Matches 833; Conservative 0; Mismatches 89; Indels 8; Gaps 4;
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1340 CTTTAAATCTCTTAATTTATCTGATTTTCTTAATTTTCTCAATTTGAAGATGAATTCCT 1399
Db 1 CTTTAAATCTCTTAATTTATCTGCAATTTCTTAATTTTCTAGATGAAGATCACTGCT 60
1400 TGTATAAAATAAGAAAAGAAATTAATCTTGAAGTAAAGCAGAGACATCATCTCTGAT 1459
Db 61 TGTATAAATAAGAAAAGAAATTAATCTTGAAGTAAAGCAGAGATGACATCATCTCTGAT 120
1460 TGTCTCTCAGCTCCCAATTTCCCAAGAG-TAAATTTCAATTTGAATTCAGCTCTGCTGCTCTG 1518
Db 121 TGCCTCTCAGCTCCCAATTTCCCAAGAGTTAAATTTCAAACTGAATTTGAGCTCTGCTGCTCTG 180
1519 GTTGGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAAGCCACTCAGGAGGAGGCTGTG 1578
Db 181 GTTGGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAAGCCACTCAGGAGGAGGCTGTG 240
1579 CTGAGTTTGTGCTGGGAATCT-CTGGGTAAAGGAACCTTAAAGAAACAAATATCATCTGCT 1637
Db 241 ATGAGTTTGTGCTGGGAATCTCTCTGGGTAAAGGAACCTTAAAGAAACAAATATCATCTGCT 300
1638 AATTC-TTTCCTAGAGGATCAGCCCTCGGATTCAGAGGATTTGGATTCAGTCTCTA 1696
Db 301 AATTCCTTCTAGAGGATCAGCCCTCGGATTTGCAAGGCTTTGGGATTCAGTCTCTA 360
1697 AGAAGCTGCTCTACTGTTGATTTGTGTCCTCAATTTCAATTTCAATTTCTTTGGAATCT 1756
Db 361 AGAAGCTGCTCTACTGTTGATTTGAAGAGTGTCCCTCGCAATTTCAATTTCTTTGGAATCT 420
1757 CAGTCTGTGAGTTTATTTGGAGATAAGGTTCTCTGAGATGTAGTTAGTTAAGCAAGGTC 1816
Db 421 CGTCTGTGAGTTTATTTGGAGATAAGGTTCTCTGAGATGTAGTTAGTTAAGCAAGGTC 480
1817 ATGCTGGATGAAGGTAGACCTTAATTTCAATTTCAATTTCAATTTCTTTGATGAAGAGAG 1876
Db 481 ATGCTGGATGAAGGTAAACCTTAATTTCAATTTCAATTTCAATTTCTTTGATGAAGAGAG 540
1877 GACACAGAGACA-----GAGGAGACGCGGGGAAGACTATGTAAGATGAAGGCAGAGATC 1931
Db 541 GACACAGAGACACAGAGGATGCGGGGAAGAGACTATGTAAGAGCAAGGCGCAGAGATA 600
1932 GGAGTTTTGACGCCCAAGCTAAGAAACACCAAGGATTTGTGCAACCATCAGAGGCTTG 1991
Db 601 GGAGTTGATGCGGCCACAGCCCAAGCAACCAAGGATTTGTGCAACCATCAGAGGCTTG 660
1992 AAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTTGAAGGATTAACGGCTCTGCTGAAC 2051
Db 661 AAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTTGAAGGATTAACGGCTCTGCTGAAC 720
2052 TTAATCTCAGACTTCCAGCTCTCAAGCAAGAAATAAATTTTCGGCTGTTTAAAGCC 2111
Db 721 TTAATCTCAGACTTCTAGCTCTCTGAATGAAGAAATAAATTTTCGACTGTTTAAAGCC 780
2112 ACCAAGGATAATTTGGTTACAGAGCTCTAGGAAACCTAATACAGCTGCTAAAATGATCCCT 2171
Db 781 ACCAAGGATAATTTGGTTTGGCAGCTCTCGAAATGAATACAGCTGCTAAAATGATCCCT 840
2172 GTCTCTCGTGTTCATTTCTGTGTGTGCTCCCTCCCAATGTATCAAAAGTTGCTTTG 2231

/db_xref="taxon:9544"
/sex="male"
/dev_stage="newborn infant"
/lab_host="E. coli SOLR"
/clone_lib="Katze.MMP2"
/note="Organ: placenta; Vector: Uni-ZAP XR; Site: 1: EcoR
1; Site: 2: Xho I; Created from Stratagene ZAP-CDNA
Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III
Gold Cloning Kit (Catalog #200450)"


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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Female"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AAGTGAAGAATTCGGCGCCGAGGAATTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo. "
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ORIGIN

Query Match 27.6%; Score 707; DB 5; Length 750;
Best Local Similarity 99.3%; Pred. No. 1.7e-171;
Matches 729; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1830 GTAGACCTAAATTCATATGACTGTTCTCTGTATGAAGGAGGACAGACAGACAG 1889
DB 1 GTAGACCTAAATTCATATGACTGTTCTCTGTATGAAGGAGGACAGACAGACAG 59
QY 1890 AGGAGACGGGGGAGAGACTATGTAAGATGAAGGACAGATCGAGTTTTCAGCCACAA 1949
DB 60 AGGAGACGGGGGAGAGACTATGTAAGATGAAGGACAGATCGAGTTTTCAGCCACAA 119
QY 1950 GCTAAGAAACACCAAGGATTTGGCAACCATCAGAGCTTGAAGAGGCAAGAGAAT 2009
DB 120 GCTAAGAAACACCAAGGATTTGGCAACCATCAGAGCTTGAAGAGGCAAGAGAAT 179
QY 2010 CTTCCCTAGAGCTTTAGAGGATACGGCTCTGCTGAACCTTAATCTCAGACTTCCAG 2069
DB 180 CTTCCCTAGAGCTTTAGAGGATACGGCTCTGCTGAACCTTAATCTCAGACTTCCAG 239
QY 2070 CTTCTGGAAGGAAAGATAATTTTCGCTGTTTTTAAGCCACCAAGGATTAATTCGTTA 2129
DB 240 CTTCTGGAAGGAAAGATAATTTTCGCTGTTTTTAAGCCACCAAGGATTAATTCGTTA 299
QY 2130 CAGCAGCTCTAGGAAACTAATCAGCTGCTAAAATGATCCCTGCTCTGTTTACAT 2189
DB 300 CAGCAGCTCTAGGAAACTAATCAGCTGCTAAAATGATCCCTGCTCTGTTTACAT 359
QY 2190 TCTGTGTGTCCTCCACCAATGACCAAGTTGCTTTGTGACCCCAATAGATATGG 2249
DB 360 TCTGTGTGTCCTCCACCAATGACCAAGTTGCTTTGTGACCCCAATAGATATGG 418
QY 2250 CAGAAGTGATGGCATGCCACTTCCAGATTAGGTTATTAAGACACTGCGCTTCTACAT 2309
DB 419 CAGAAGTGATGGCATGCCACTTCCAGATTAGGTTATTAAGACACTGCGCTTCTACAT 478
QY 2310 GAGCCCTCTCTCTGCCCCACCCACCCCAATCTATCTTGCTCACTCGCTCTGGGGG 2369
DB 479 GAGCCCTCTCTCTGCCCCACCCACCCCAATCTATCTTGCTCACTCGCTCTGGGGG 538
QY 2370 AAGCTAGCTGCCATGCTATGAGCAGCGCTTATAAGAGACTTACGTGGTAAAAAATGAAT 2429
DB 539 AAGCTAGCTGCCATGCTATGAGCAGCGCTTATAAGAGACTTACGTGGTAAAAAATGAAT 598
QY 2430 CTTCCCTGCCACAGCCACATTTAGTGAACCTAGAGCAGAGACTCTGAGATTAATCGATGT 2489
DB 599 CTTCCCTGCCACAGCCACATTTAGTGAACCTAGAGCAGAGACTCTGAGATTAATCGATGT 658
QY 2490 TTGTTGTTTTAAAGTTGCTCAGTTTTCGTTCTAACTGTTATGACGCAATAGATAAATAA 2549
DB 659 TTGTTGTTTTAAAGTTGCTCAGTTTTCGTTCTAACTGTTATGACGCAATAGATAAATAA 718
QY 2550 TGCAGAGAAAGAGA 2563
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Db 719 TGCAGAGAAAGAGA 732

RESULT 7
BI089828
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI089828 726 bp mRNA linear EST 20-JUN-2001
602855071F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996432 5',
mRNA sequence.
BI089828
BI089828.1 GI:14508158
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 726)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM11021 row: n column: 17
High quality sequence stop: 709.
Location/Qualifiers
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 Kb. Library prepared by Life
Technologies."

FEATURES
source

ORIGIN

Query Match 26.7%; Score 683.8; DB 4; Length 726;
Best Local Similarity 98.1%; Pred. No. 1.7e-165;
Matches 713; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 40 GTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATA 99
DB 1 GTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATA 60
QY 100 ACCAGCTTCTAGCTGGAGGGCTGCATGTCAGGGAAGTCAATTAAGGTGAAGAGATCAGCG 159
DB 61 ACCAGCTTCTAGCTGGAGGGCTGCATGTCAGGGAAGTCAATTAAGGTGAAGAGATCAGCG 120
QY 160 TGGTCCCCCAATCGGTGGCTGGATGCCAGCTGTCCCCGTCTATCTGGGTGCCAGGGTG 219
DB 121 TGGTCCCCCAATCGGTGGCTGGATGCCAGCTGTCCCCGTCTATCTGGGTGCCAGGGTG 180
QY 220 GAAGCAGTGCCTGTCTCATGTGGGGTGGGGCAGGAGCCGACTCTAAACACTAGAGCCAGTGA 279
DB 181 GAAGCAGTGCCTGTCTCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGA 240
QY 280 ACATCATGAGCTCTATCTTTGTGTGCAAGGAATCCAAGAGCTTCACTTCTACCGGGGG 339
DB 241 ACATCATGAGCTCTATCTTTGTGTGCAAGGAATCCAAGAGCTTCACTTCTACCGGGGG 300
QY 340 ACATGGGGCTACCTCCAGCTTCGAGTCGGCTTACCCGGGCTGGTTCCTGTGTCACGG 399
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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 702)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-61, sAT-rich#Low_complexity
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
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 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_Ftl"
 /note="Organ: Lung; Vector: pVT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP Ftl is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pVT73-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 GCCCATGCCG. The tissue was provided by Dr. Gary W.
 Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-Ftl
 TAG_SEQ=GGCCATGCCG"

ORIGIN
 Query Match 25.2%; Score 644.6; DB 6; Length 702;
 Best Local Similarity 97.4%; Pred. No. 2.4e-155;
 Matches 675; Conservative 0; Mismatches 16; Indels 2; Gaps 2;
 587 GCTCTCAGGACCCCGCTGACTAGTGGGACCTGACCACTTGTCTTCTGGTTCCC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 702 GCTCTCAGGACCCCGCTGACTAGTGGGACCTGACCACTTGTCTTCTGGTTCCC 643
 Qy 647 AGTTTGCATAAATCTGAGATTTGGAGCTCAGTCAGGCTCTCCCCCACTGATGGTGC 706
 Db 642 AGTTTGCATAAATCTGAGATTTGGAGCTCAGTCAGGCTCTCCCCCACTGATGGTGC 584
 Qy 707 TACTGCTGGNACCTTGTAAACCAATGCGGTAAACTGGGAATAACATGAAGAATT 766
 Db 583 TACTGCTGGNACCTTGTAAACCAATGCGGTAAACTGGGAATAACATGAAGAATT 524
 Qy 767 TCTGTGGGGGTGGGGTGGGGAGTCTGGGAATCAATCTCTGCTTAATGTAACATGACAAG 826
 Db 523 TCTGTGGAGGTGGGGTGGGGAGTCTGGGAATCAATCTCTGCTTAATGTAACATGACCAG 464
 Qy 827 TGTTACCTGAGCCCGCCAGGCAACCCATCCCACTGAGCTTATAGGGTCAGTAGCT 886
 Db 463 TGTTACCTGAGCCCGCCAGGCAACCCATCCCACTGAGCTTATAGGGTCAGTAGCT 404
 Qy 887 CTCACATGAGTCTCTCACTCACCACCTGTGCAGAGAGGAGGTGTCATAGAGTCAG 946
 Db 403 CTCACATGAGTCTCTCACTCACCACCTGTGCAGAGAGGAGGTGTCATAGAGTCAG 344
 Qy 947 GGATCTATGGCCCTTGGCCCGACCCCTTCCCTTT-ATCCTGCCACTGTCTATATG 1005
 Db 343 GGATCTATGGCCCTTGGCCCGACCCCTTCCCTTTATCTGCCACTGTCTATATG 284
 Qy 1006 CTACCTTTCTATCTCTTCCCTCATCTCTTGTGGGCATGAGAGGTGCTGATGCTCA 1065
 Db 283 CTACCTTTCTATCTCTTCCCTCATCTCTTGTGGGCATGAGAGGTGCTGATGCTCA 224
 Qy 1066 GAAGAATGTTGAGCTCAGAGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTAA 1125
 Db 223 GAAGAATGTTGAGCTCAGAGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTAA 164
 Qy 1126 AAACCCAGATACAAATCCAGATGCTGCTCTCTATTCCCATGAAAAGTCTCTCA 1185
 Db 163 AAACCCAGATACAAATCCAGATGCTGCTCTCTATTCCCATGAAAAGTCTCTCA 104
 Qy 1186 TGACATATTGAGAAGACCTTACTTACAAAGTGCATATATTGCAATTTATTTAATTTAAA 1245
 Db 103 TGACATATTGAGAAGACCTTACTTACAAAGTGCATATATTGCAATTTATTTAATTTAAA 44
 Qy 1246 GATACCTATTATATTTCTTTTATAGAAAAA 1278
 Db 43 GATACCTATTATATTTCTTTTATAGAAAAA 11

RESULT 10
 BF509095/c
 LOCUS
 DEFINITION
 BF509095
 IMAGE:3086280 3', mRNA sequence.
 VERSION
 BF509095.1 GI:11592393
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 697)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 NCI-CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive

elements were found in this cDNA sequence: 1-60,

>AT rich#Low complexity

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..697

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3086280"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_Sub8"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub8

is a subcloned library derived from NCI CGAP Subs. The

NCI CGAP Sub8 library had 2.5 million recombinants. A

single-stranded DNA preparation of NCI_CGAP Subs was used

as a tracer in a subtractive hybridization with a driver

comprising: a pool of clones from NCI CGAP Subs (IMAGE

clone Ids 2732833-2737415, 3068040-3069191; 25% of the

driver population), a pool of clones from NCI CGAP Sub4

(IMAGE clone Ids 2723592-2729326; 25% of the driver

population), NCI CGAP Sub6 (pool AIF-AJU, IMAGE Ids

2728969-2733190; 25% of the driver population), and

NCI CGAP Sub7 (IMAGE Ids 3069192-3072238,

3081864-3084550; 25% of the driver population).

Subtraction was performed as previously described

[Bonaldo, Lennon & Soares (1996): Normalization and

Subtraction: Two Approaches To Facilitate Gene Discovery.

Genome Research 6, 791-806.

TAG TISSUE=lung

TAG LIB=NCI CGAP_Lu19

TAG_SEQ=GACAGC"

ORIGIN

Query Match 25.1%; Score 643.2; DB 2; Length 697;

Best Local Similarity 97.7%; Pred. No. 5.6e-155;

Matches 673; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 591 TCAGGACCCCGAGTCTGACTTAGTGGGACCTGACCACTTTGCTCTGTTCCAGTT 650

DB 697 TCAGGACCCCGAGTCTGACTTAGTGGGACCTGACCACTTTGCTCTGTTCCAGTT 638

QY 651 TGCATAAATCTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCACTGGATGCTACT 710

DB 637 TGGATAAATCTGAGATTT-GAGCTCAGTCCAGGGTCTCTCCCACTGGATGCTACT 579

QY 711 GCTGTGGAACCTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTCTG 770

DB 578 GCTGTGGAATCTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTCTG 519

QY 771 TGGGGTGGGGTGGGGAGTGTGGGAATCATTCCTGTTAATGGTAACTGACCAAGTT 830

DB 518 TGGAGTGGGGTGGGGAGTGTGGGAATCATTCCTGTTAATGGTAACTGACCAAGTT 459

QY 831 ACCCTGAGCCCGCAGGCCAACCCCTCCAGTTGAGCCCTTATAGGGTCAGTAGCTCTCC 890

DB 458 ACCCTGAGCCCGCAGGCCAACCCCTCCAGTTGAGCCCTTATAGGGTCAGTAGCTCTCC 399

QY 891 ACATGAAGTCTCTCATCTACCACTGTGAGGAGGGAGGGTGGTTCATAGATCAGGGAT 950

DB 398 ACATGAAGACCTGTCTACTCACCCTATGAGGAGGGAGGGTGGTTCATAGATCAGGGAT 339

QY 951 CTATGSCCTTGGCCAGCCCAACCCCTTCCCTTT-ATCCTGCCACTGTCTATATGCTAC 1009

DB 338 CTATGSCCTTGGCCAGCCCAACCCCTTCCCTTTAATCCTGCCACTGTCTATATGCTAC 279

QY 1010 CTTTCCTATCTCTTCCCTCATCATCTTGTGTGGCATCAGGAGGTGGTGTCTCAGAG 1069

DB 278 CTTTCCTATCTCTTCCCTCATCATCTTGTGTGGCATCAGGAGGTGGTGTCTCAGAG 219

QY 1070 AAATGGTTCGAGTCTAGAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAAC 1129

DB 218 AAATGGTTCGAGTCTAGAGATAAAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAAC 159

QY 1130 CCAAGATACAATCAAAATCCCAAGATCGTGGTCTCTATTCCCAATGAAAAAGTCTCATGAC 1189

DB 158 CCAAGATACAATCAAAATCCCAAGATCGTGGTCTCTATTCCCAATGAAAAAGTCTCATGAC 99

QY 1190 ATATTGAGAAGACCTACTTACAAAGTGCATATATTGCAATTTATTTTAAATAAGATA 1249

DB 98 ATATTGAGAAGACCTACTTACAAAGTGCATATATTGCAATTTATTTTAAATAAGATA 39

QY 1250 CCTATTATATATTTCTTTATAGAAAAA 1278

DB 38 CCTATTATATATTTCTTTATAGAAAAA 10

RESULT 11

BI090567

LOCUS

DEFINITION

602855674F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996939 5',

mrna sequence.

ACCESSION

BI090567

VERSION

BI090567.1 GI:14508897

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 858)

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

AUTHORS

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1023 row: c column: 20

High quality sequence stop: 670.

Location/Qualifiers

1..858

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4996939"

/cell_line="MGC36"

/lab_host="DH10B"

/clone_lib="NIH MGC 10"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5 kb. Library prepared by Life

Technologies."

ORIGIN

Query Match 24.6%; Score 631.6; DB 4; Length 858;

Best Local Similarity 91.9%; Pred. No. 5.9e-152;

Matches 689; Conservative 0; Mismatches 59; Indels 2; Gaps 2;

QY 1 AGGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCAGTGGGGCGTGTCTTCCGAA 60

DB 106 AGGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCAGTGGGGCGTGTCTTCCGAA 165

QY 61 TGAAGACTCGGCATTTGAGGTCTTTATCTGCATAATAACCACTTCTAGCTGAGGGC 120

DB 166 TGAAGACTCGGCATTTGAGGTCTTTATCTGCATAATAACCACTTCTAGCTGAGGGC 225

QY 121 TGCATGCGAGGAGGTCTATTAAGGTGAAGATCAGGTGGTCCCAATCGTGGCTGG 180

DB 226 TGCATGCGAGGAGGTCTATTAAGGTGAAGATCAGGTGGTCCCAATCGTGGCTGG 285

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QY 181 ATGCCAGCCTGTCCCGCTCATCTCGGTGTCCAGGTTGGAAGCCAGTGCCTGTCATGTG 240
Db 286 ATGCCAGCCTGTCCCGCTCATCTCGGTGTCCAGGTTGGAAGCCAGTGCCTGTCATGTG 345
QY 241 GGGTGGGAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTG 300
Db 346 GGGTGGGAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTG 405
QY 301 GTGCCAAGAAATCAAGAGTTTCACTTCTACCGGGGGAGACATGGGGCTCACTCCAGCT 360
Db 406 GTGCCAAGAAATCAAGAGTTTCACTTCTACCGGGGGAGACATGGGGCTCACTCCAGCT 465
QY 361 TCGAGTGGCTGCTTACCCGGGCTGCTCTGTGCAAGCTGCTGAGCCGATCAGCCTG 420
Db 466 TCGAGTGGCTGCTTACCCGGGCTGCTCTGTGCAAGCTGCTGAGCCGATCAGCCTG 525
QY 421 TCAGACTCACCCAGCTTCCCGAAGATGGTGGTGGATGCCCATCAGAGCTTCTACT 480
Db 526 TCAGACTCACCCAGCTTCCCGAAGATGGTGGTGGATGCCCATCAGAGCTTCTACT 585
QY 481 TCAGAGTGTGACTAGGGAACGTCGCCGCCGCCAGAACTCCCTGGGAGAGCCAGCTCGG 540
Db 586 TCAGAGTGTGACTAGGGAAC-AGTGCCCCCAGAACTCCCTGGGAGAGCCAGCTCGG 644
QY 541 GTGAGGGTGTGAGGAGAGCCATGCGGGGAGAACTCACTTCTTCTGCTCTCAGGACCC 600
Db 645 GTGAGGGTGTGAGGAGAGCCATGCGGGGAGAACTCACTTCTTCTGCTCTCAGGACCC 704
QY 601 CAGGCTGACTTAGTGGGACCTGACCACTTCTTCTGCTTCTGCTTCCAGTTTGCATAAAT 660
Db 705 CA-GTCTGACTTAGAGGGAACCTGACAACTTGGCTTCTGGTCCAGTTTGGATATCT 763
QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCACTGGATGGTGTCTGCTGTGGAAC 720
Db 764 GACAAATAGAGCTCCAGGTCACGGTACTCCAGAAATGGATGGAGCTACTGGTGTGGAAC 823
QY 721 CTGTGAAAAACCAATGTGGGTAACCTGGGA 750
Db 824 CGTTGAAAAACCAATGTGGGTAACCAAGGA 853

RESULT 12
BX350083/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BX350083 915 bp mRNA linear EST 23-APR-2004
BX350083 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1013YA07 3-PRIME, mRNA sequence.
BX350083
BX350083.2 GI:46553561
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 915)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30383465.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1383.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS08A1018D02_CS01644_2&c=1383.f

FEATURES
source
1. .915
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1013YA07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 21.5%; Score 551.4; DB 5; Length 915;
Best Local Similarity 87.0%; Pred. No. 3.6e-131;
Matches 617; Conservative 0; Mismatches 91; Indels 1; Gaps 1;

QY 915 TGTGAGGAGAGGAGGAGTGTGTCATAGTCAAGGATCTATGGCCCTTGGCCAGCCAC 974
Db 709 TCTATAGAGTCAAGGTTTAAATGCCCCCTTGGGCCCAAGCCCCCCTTTCCCTT 650
QY 975 CCCCCCTTTCATCTGCCACTGTCTATGTCATCTTCTTCTTCTTCTTCTTCTTCTTCT 1034
Db 649 TTAATCCCTGCCACTGTCAAAATGCTAACTTCTTCTTCTTCTTCTTCTTCTTCTTCT 590
QY 1035 TTGTTGTGGCATGAGGAGTGGTGTGTCAG-AAGAAATGGTTCGAGCTCAGAAGATA 1093
Db 589 GGTGTGGGCATGAGGAGGAGTGTGTCAGAAAGAAATGGCTCGAGCTCAGAAGATA 530
QY 1094 AAGATAAGTAGGATGTGCTGATCCCTCTTTTAAACCAGAGATACAAATCAAAATCCAGA 1153
Db 529 AAGATAAGTAGGATGTGCTGATCCCTCTTTTAAACCAGAGATACAAATCAAAATCCAGA 470
QY 1154 TGCTGTCTTCTATTCCTATGAAAGTGTCTATGACATATTTGAGAGAGACTTACTTACAA 1213
Db 469 TGCTGTCTTCTATTCCTATGAAAGTGTCTATGACATATTTGAGAGAGACTTACTTACAA 410
QY 1214 GTGGCATATTTGCAATTTTAAATTAAGATACCTTATTTATATATTTCTTTATAGA 1273
Db 409 GTGGCATATTTGCAATTTTAAATTAAGATACCTTATTTATATATTTCTTTATAGA 350
QY 1274 AAAAGTCTGGAAGAGTTTACTTCAATCTAGCAATGTGAGGTGTGGCAGTATAGGTG 1333
Db 349 AAAAGTCTGGAAGAGTTTACTTCAATGTAGCAATGTGAGGTGTGGCAGTATAGGTG 290
QY 1334 ATTTTCTTTTAAATCTGTTAAATTTATCTGATTTTCTTAAATTTTCTTAAATGAAGATGA 1393
Db 289 ATTTTCTTTTAAATCTGTTAAATTTATCTGATTTTCTTAAATTTTCTTAAATGAAGATGA 230
QY 1394 ATCTCTGTATATAAATAAGAAAGAAATTAATCTTGTAGGTAAAGAGAGAGAGATCATC 1453
Db 229 ATCTCTGTATATAAATAAGAAAGAAATTAATCTTGTAGGTAAAGAGAGAGATCATC 170
QY 1454 TCTGATTTGCTCAGCTCCAAATTTCCAGAGATTAATTTCAAAATTTGAATTCGAGCTGTGCTG 1513
Db 169 TCTGATTTGCTCAGCTCCAAATTTCCAGAGATTAATTTCAAAATTTGAATTCGAGCTGTGCTG 110
QY 1514 CTCTGTTGTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1573
Db 109 CTCTGTTGTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 50
QY 1574 CTGTGCTGAGTTTGTGTGCTGGAATCTCTGGTAAAGAACTTAAAGAA 1622
Db 49 CTGTGATGAGTTTGTGTGCTGGAATCTCTGGTAAAGAACTTAAAGAA 1

RESULT 13
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AUI138695 555 bp mRNA linear EST 02-AUG-2002
AUI138695 PLACEN1 Homo sapiens cDNA clone PLACE1009110 5', mRNA
sequence.
AUI138695
AUI138695.1 GI:11000216
VERSION
KEYWORDS
EST.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 555)
AUTHORS Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
          Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
          Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
          Genomics Laboratory
          Helix Research Institute
          1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: genomics@hri.co.jp
          HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
          Research Institute; cDNA library construction: Department of
          Virology, Institute of Medical Science, University of Tokyo, and
          Helix Research Institute.
FEATURES             Location/Qualifiers
     source           1..555
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="PLACE1009110"
                     /tissue_type="placenta"
                     /clone_lib="PLACE1"
                     /note="Vector: pME18SFL3"

ORIGIN
Query Match       20.6%; Score 527.8; DB 1; Length 555;
Best Local Similarity 97.8%; Pred. No. 4.1e-125;
Matches 543; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 695 ACTGGATGGTCTACTGTGGAACCTTGTAAAAACCATGTGGGTAACTGGGAATAA 754
DB 1 ACTGGATGGTCTACTGTGGAACCTTGTAAAAACCATGTGGGTAACTGGGAATAA 60
QY 755 CATGAAAGATTCTGTGGGGTGGGGAGTGGTGGGAATCATCTTCCTTAATG 814
DB 61 CATGAAAGATTCTGTGGGGTGGGGAGTGGTGGGAATCATCTTCCTTAATG 120
QY 815 GTAACGTACAAGTGTACCTGAGCCCGCAGGCCAACCCATCCCCAGTTGAGCCTTATA 874
DB 121 GTAACGTACAAGTGTACCTGAGCCCGCAGGCCAACCCATCCCCAGTTGAGCCTTACA 180
QY 875 GGGTCAGTAGCTCCACATGAAGTCTCTCACTACCACTGTCAGGAGAGGGAGGTGG 934
DB 181 GGGTCAGTAGCTCCACATGAAGTCTCTCACTACCACTGTCAGGAGAGGGAGGTGG 240
QY 935 TCATAGAGTCAGGATCTATGGCCCTTGGCCAGCCGCCACCCCTTCCCTTT-ATCCTGC 993
DB 241 TCATAGAGTCAGGATCTATGGCCCTTGGCCAGCCGCCACCCCTTCCCTTTAATCCTGC 300
QY 994 CACTGTCATATGCTACTCTTCCCTATCTCTTCCCTCATCATCTTGTGTGGGATGAGGAG 1053
DB 301 CACTGTCATATGCTACTCTTCCCTATCTCTTCCCTCATCATCTTGTGTGGGATGAGGAG 360
QY 1054 GTGGTGATGTCAAGAAATGGTTCCAGCTCAGAGATAAAGATAAGTAGGATGCTG 1113
DB 361 GTGGTGATGTCAAGAAATGGTTCAGCTCAGAGATAAAGATAAAGTAGGATGCTG 420
QY 1114 ATCCCTCTTTAAACCCAGATACATCAATCCAGATCGTGTCTTATCCCATG 1173
DB 421 ATCCCTCTTTAAACCCAGATACATCAATCCAGATCGTGTCTTATCCCATG 480
QY 1174 AAAAAAGTGTCTGACATATTTGAGAAGACCTACTTACAAAGTGGCATATATTTGCAATTTA 1233
DB 481 AAAAAAGTGTCTGACATATTTGNAANAACCTACTTACAAAGTGGCATATATTTGCAATTTA 540
QY 1234 TTTTAATTTAAAGAT 1248

Db 541 TTTTAATTTAAAGAT 555

RESULT 14
BQ351235
LOCUS RC0-HT0773-010600-021-e07 HT0773 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ351235
ACCESSION BQ351235
VERSION BQ351235.1 GI:21015291
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 555)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
          Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
          Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
          O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
          Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC0&t2=RC0-HT0773-
          010600-021-e07&t3=2000-06-01&t4=1)
          Seq primer: puc 18 forward
          High quality sequence start: 14
          High quality sequence stop: 555.
          Location/Qualifiers
             1..555
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /dev_stage="Adult"
             /clone_lib="HT0773"
             /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORESTES PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the puc 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."

ORIGIN
Query Match       18.8%; Score 481; DB 5; Length 555;
Best Local Similarity 98.6%; Pred. No. 5.5e-113;
Matches 506; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1792 AGATGTAGTTAGTAAACAAGTCTGTCGATGAAGTAGACC-TAAATTCATATGA 1850
DB 27 AGATATAGTGTAGTAAACAAGTCTGTCGATGAAGTAGACCCTAAATTCATATGA 86
QY 1851 CTGGTTTCCTTGTATGAAAAAGAGAGGACACAGACAGAGGAGCGGGGAAGACTAT 1910
DB 87 CTGGTTTCCTTGTATGAAAAAGAGAGGACACAGACAGAGGAGTGGGGGAAGACTAT 146
QY 1911 GTAAAGATGAAGCGAGAGATCGAGCTTTTGGCAGCCACAAGCTTAAGAAACACCAAGATTG 1970
DB 147 GTAAAGATGAAGCGAGAGATCGAGCTTTTGGCAGCCACAAGCTTAAGAAACACCAAGATTG 206
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QY 1971 TCGCACCATCAGACGCTTGGAGAGGCAAGAGAAATTTCTCCCTAGAGGCTTTAGAGG 2030
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
207 TGGCAACCATCAGAAGCTTGGAGAGGCAAGAGAAATTTCTCCCTAGAGGCTTTAGAGG 266
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2031 GATAACGGCTCTGCTGAAACCTTAAATCTCAGACTTCCAGCCTCCTGAACGAAGAAGAAT 2090
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
267 GATAACGGCTCTGCTGAAACCTTAAATCTCAGACTTCCAGCCTCCTGAACGAAGAAGAAT 326
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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327 AAATTCGGCTGTTTAAAGCCCAAGGATAATTTGGTTACAGAGCTCTAGGAACTAAT 386
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QY 2151 ACAGCTGCTAAATGATCCCTGCTCTCTGCTGTTTACATCTCTGCTGCTCCCTCCAC 2210
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387 ACAGCTGCTAAATGATCCCTGCTCTCTGCTGTTTACATCTCTGCTGCTCCCTCCAC 446
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2211 AATGTACCAAAAGTTGCTTTTGTGACCAATAGATAATGCGAAGTGATGCGCATGCCACT 2270
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
447 AATGTACCAAAAGTTGCTTTTGTGGA-CCATAGATATGCGAAGTGATGCGCATGCCACT 505
QY 2271 TCCAAGATTAGTTTATAAAGACACTGCAGCTT 2303
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
506 TCCAAGATTAGTTTATAAAGACACTGCAGCCT 538
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RESULT 15
LOCUS AY413262
DEFINITION Homo sapiens IL1F5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY413262
VERSION AY413262.1 GI:39769224
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 468)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 468)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>468
/gene="IL1F5"
/locus_tag="HCM4832"
ORIGIN
Query Match 18.3%; Score 468; DB 9; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.2e-109;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 ATGGTCTCAGTGGGCGCTGTGCTTCCGAATGAAGACTTCGGCATTTGAAGTGCTTTAT 89
|||||
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QY 90 CTGCATAATAACACGCTTCTAGCTGAGGGCTGCATGCGAGGGAAGTCAATTAAGTGAA 149
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61 CTGCATAATAACACGCTTCTAGCTGAGGGCTGCATGCGAGGGAAGTCAATTAAGTGAA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 150 GAGATCAGGCTGGTCCCAATCGGTGGGATGCCAGCCTGTGCCCGCTCATCTCTGGGT 209
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GAGATCAGGCTGGTCCCAATCGGTGGGATGCCAGCCTGTGCCCGCTCATCTCTGGGT 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 210 GTCCAGGGTGGAAAGCCAGTGCCTGTCTCATGTGGGGTGGGCGAGGAGCCGACTCTAAACACTA 269
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GTCCAGGGTGGAAAGCCAGTGCCTGTCTCATGTGGGGTGGGCGAGGAGCCGACTCTAAACACTA 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 270 GAGCAGTGAACATCATGAGAGCTCTATCTTGTGCGCAAGGAATCCAGAGCTTCACCTTC 329
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GAGCAGTGAACATCATGAGAGCTCTATCTTGTGCGCAAGGAATCCAGAGCTTCACCTTC 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 330 TACCGCGGGGACATGGGGCTCACCTCCAGCTTCGAGTGGGCTGCTTACCGGGCTGGTTC 389
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TACCGCGGGGACATGGGGCTCACCTCCAGCTTCGAGTGGGCTGCTTACCGGGCTGGTTC 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 390 CTGTGCACGGTGCCTGAAGCCGATCAGCCTGTCTCAGACTCACCCAGCTTCCCGAGAAATGGT 449
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CTGTGCACGGTGCCTGAAGCCGATCAGCCTGTCTCAGACTCACCCAGCTTCCCGAGAAATGGT 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 450 GGCTGGAATGCCCCCATCAAGACTTCTTACTTCCAGCAGTGTGACTAG 497
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 GGCTGGAATGCCCCCATCAAGACTTCTTACTTCCAGCAGTGTGACTAG 468
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: March 13, 2005, 18:13:41
Job time : 8398.03 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 10:45:20 ; Search time 21.27 Seconds
(without alignments)
10854.228 Million cell updates/sec

Title: US-09-617-720A-2
Perfect score: 39
Sequence: 1 ttgaggacagcagactccacagctccgccagagaa 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
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4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
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9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	AAF27922	Aaf27922 Human IL-
2	37.4	95.9	54	AAF27927	Aaf27927 Interleuk
3	37.4	95.9	2720	ADN05043	Adn05043 Antipsori
4	37.4	95.9	5751	AAF31355	Aaf31355 Genomic c
5	37.4	95.9	5751	ABZ77450	Abz77450 Genomic D
6	37.4	95.9	5752	AAZ30052	Aaz30052 DNA encod
7	37.4	95.9	6540	AAF27950	Aaf27950 Interleuk
8	37.4	95.9	7605	AAZ30053	Aaz30053 DNA encod
9	37.4	95.9	7605	AAF31356	Aaf31356 Extension
10	37.4	95.9	7605	ABZ77451	Abz77451 Extended
11	22.8	58.5	3071	ABL26414	Ab126414 Drosophil
12	22.6	57.9	49087	ACN44492	Acn44492 Mouse gen
13	22.4	57.4	689	AAK61778	Aak61778 Human imm
14	22.4	57.4	7667	AAZ27743	Aaz27743 DNA encod
15	22.4	57.4	7667	AAK82163	Aak82163 Human imm
16	22.4	57.4	7667	AAK80991	Aak80991 Human imm
17	22.4	57.4	7667	ADB94546	Adb94546 Novel hum
18	22.4	57.4	38764	ADA03020	Ada03020 Human RAC
19	22.4	57.4	38764	ADB72758	Adb72758 Human RAC
20	22.4	57.4	38764	ADC85500	Adc85500 Human Rac

C 21	22.4	57.4	38764	12	ADM74615	Adm74615 Human ear
C 22	22.2	56.9	378	9	ACH47270	Ach47270 Human inf
C 23	22	56.4	98546	11	ACN44790	Acn44790 Human gen
C 24	21.6	55.4	1311	5	AAS67806	Aas67806 DNA encod
C 25	21.6	55.4	1830	5	AAS67805	Aas67805 DNA encod
C 26	21.6	55.4	2100	5	AAS67805	Aas67805 DNA encod
C 27	21.6	55.4	2100	5	AAS67805	Aas67805 DNA encod
C 28	21.6	55.4	2100	10	ADP69161	Adp69161 Human MP5
C 29	21.6	55.4	5397	4	ABL20241	Ab120241 Drosophil
C 30	21.6	55.4	28491	4	ABL20240	Ab120240 Drosophil
C 31	21.4	54.9	1092	5	AAS81578	Aas81578 DNA encod
C 32	21.2	54.9	276820	11	ADP75188	Adp75188 Human ADA
C 33	21.2	54.4	2064	10	ADB62042	Adb62042 Human cDN
C 34	21.2	54.4	5159	8	ACC46691	Acc46691 Human dit
C 35	21.2	54.4	6020	12	ADJ12607	Adj12607 DNA fragm
C 36	21.2	54.4	110000	13	ABD32780_3	Abd32780_3 Continuat
C 37	21.2	54.4	11441	12	ADQ21090	Adq21090 Human sof
C 38	21	53.8	391	3	AAC02974	Aac02974 Human sec
C 39	21	53.8	913	6	ABL48933	Ab148933 Ovarian c
C 40	21	53.8	1549	6	ABK49709	Abk49709 cDNA enco
C 41	21	53.8	2487	9	ACD26637	Acd26637 Human sec
C 42	21	53.8	2490	3	AAZ50813	Aaz50813 Human TAN
C 43	21	53.8	11646	4	ADQ98220	Adq98220 Human ext
C 44	21	53.8	14148	4	AAK70925	Aak70925 Human imm
C 45	20.8	53.3	1272	4	AAH99081	Aah99081 Human EST

ALIGNMENTS

RESULT 1
AAF27922
ID AAF27922 standard; cDNA; 39 BP.
XX
AC AAF27922;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human IL-1L1 coding sequence 5' end #1.
XX
KW Human; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
KW osteoporosis; systemic lupus erythematosus; ss.
XX
OS Homo sapiens.
XX
PN WO200105974-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-US019508.
XX
PR 16-JUL-1999; 99US-0144298P.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Nicklin M, Barton J;
XX
DR WPI; 2001-091974/10.
XX
PT Nucleic acids encoding human and murine interleukin-1L1 polypeptides
XX
PS useful for controlling inflammatory processes.
XX
PS Claim 20; Fig 1; 150pp; English.

The present invention provides the protein and coding sequences of the human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is located between the IL-1beta and IL-1receptor genes at human chromosome 2q13. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,

CC severe periodontal disease and pregnancy complications. The present
CC sequence is one of two alternative 5' ends of the human IL-1L1 coding
CC sequence

XX Sequence 39 BP; 12 A; 12 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39
DB 1 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39

RESULT 2
AAF27927
ID AAF27927 standard; DNA; 54 BP.
AC AAF27927;
XX 08-MAY-2001 (first entry)
DE Interleukin-1L1 coding sequence fragment #2.
XX Human; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
KW Chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
KW osteoporosis; systemic lupus erythematosus; ds.
XX Unidentified.
OS WO200105974-A2.
PN 25-JAN-2001..
XX 17-JUL-2000; 2000WO-US019508.
XX 16-JUL-1999; 99US-0144298P.
XX (INTE-) INTERLEUKIN GENETICS INC.
PI Nicklin M, Barton J;
XX WPI; 2001-091974/10.
DR Nucleic acids encoding human and murine interleukin-1L1 polypeptides
PT useful for controlling inflammatory processes.
XX Example; Fig 10; 150pp; English.

CC The present invention provides the protein and coding sequences of the
CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
CC located between the IL-1beta and IL-1receptor genes at human chromosome
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
CC of heart disease, cancer and inflammatory diseases such as rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
CC severe periodontal disease and pregnancy complications. The present
CC sequence is an IL-1L1 coding sequence fragment

XX Sequence 54 BP; 17 A; 14 C; 16 G; 7 T; 0 U; 0 Other;
Query Match 95.9%; Score 37.4; DB 5; Length 54;
Best Local Similarity 97.4%; Pred. No. 0.00027;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39
DB 2 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 40

RESULT 3

ADN05043
ID ADN05043 standard; cDNA; 2720 BP.
XX AC ADN05043;
XX 01-JUL-2004 (first entry)
DT Antipsoriatic cDNA sequence #737.
DE ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
KW Homo sapiens.
OS WO2004028479-A2.
XX 08-APR-2004.
PD 25-SEP-2003; 2003WO-US030907.
PF 25-SEP-2002; 2002US-0414006P.
PR (GETH) GENENTECH INC.
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu ID;
XX WPI; 2004-305105/28.
DR P-PSDB; ADN05044.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX Claim 1; SEQ ID NO 1437; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.

XX Sequence 2720 BP; 735 A; 621 C; 671 G; 693 T; 0 U; 0 Other;
Query Match 95.9%; Score 37.4; DB 12; Length 2720;
Best Local Similarity 97.4%; Pred. No. 0.0004;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39
DB 83 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 121

RESULT 4
AAF31355
ID AAF31355 standard; DNA; 5751 BP.
XX AAF31355;
XX 05-APR-2001 (first entry)
DT Genomic clone B2HFLS20W.
XX Interleukin; IL-1 receptor; cancer; inflammation; ds.
XX Homo sapiens.
XX WO200102571-A2.
XX 11-JAN-2001.
XX 07-JUL-2000; 2000WO-US018710.
XX 07-JUL-1999; 99US-00348942.

PR 13-OCT-1999; 99US-00417455.
PR 08-DEC-1999; 99US-00457626.
PR 10-MAR-2000; 2000US-00523552.
PR 22-MAY-2000; 2000US-00576008.
XX (HYSE-) HYSEQ INC.
XX Ford J, Pace A;
XX WPI; 2001-071582/08.
DR WPI; 2001-071582/08.
XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
PT proteins (referred as IL-1Hv1), useful in the treatment of cancer, e.g.
PT breast adenocarcinoma and brain tumors, and an inflammatory disease
PT mediated by IL-18.
XX Claim 1; Fig 9; 179pp; English.
XX The present invention relates to interleukin (IL)-1 receptor antagonist
CC proteins. IL-1Hv1 is useful for treating cancer, an inflammatory disease
CC mediated by IL-18, inflammation resulting from infection or allergic
CC reactions, and inflammation associated with chronic bronchitis,
CC arthritis, diabetes or endothermia
XX Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;
SQ Query Match 95.9%; Score 37.4; DB 4; Length 5751;
Best Local Similarity 97.4%; Pred. No. 0.00043;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTGAGGACAGCAGACTCCACAGCTCCCGCCAGGAGAA 39
DB 813 TGGAGGACAGCAGACTCCACAGCTCCCGCCAGGAGAA 851
RESULT 5
ABZ77450
ID ABZ77450 standard; cDNA; 5751 BP.
XX AC ABZ77450;
XX 28-MAY-2003 (first entry)
XX Genomic DNA sequence of a human Interleukin-1Hv1 (IL-1Hv1).
XX Interleukin-1Hv1; IL-1Hv1; B-cell proliferation; B-cell activation;
KW B-cell differentiation; B-cell-related disorder; lymphoma; leukemia;
KW myeloma; infection; autoimmune disease; allergy; asthma;
KW allergic rhinitis; IGA production; ss.
XX Homo sapiens.
XX WO2003010291-A2.
XX 06-FEB-2003.
XX 25-JUL-2002; 2002WO-US023845.
XX 25-JUL-2001; 2001US-0307754P.
PR 29-NOV-2001; 2001US-0334668P.
XX (HYSE-) HYSEQ INC.
XX Ho AS, Lin H, Ford JE, Rupp F;
XX WPI; 2003-239438/23.
XX Inhibiting or stimulating B-cell proliferation, activation or
PT differentiation, useful for treating B-cell-related disorders or
PT autoimmune diseases, comprises administering an interleukin-1Hv1
PT polypeptide or its inhibitor.
XX Disclosure; Page 109-111; 115pp; English.

XX The present sequence encodes human interleukin (IL)-1Hv1 polypeptide. IL-
CC 1Hv1 inhibitors are used in the method of the invention. The
CC specification describes a method of inhibiting B-cell proliferation,
CC activation or differentiation. The method comprises administering an
CC inhibitor of IL-1Hv1 activity to a human with elevated B-cell levels or
CC activity, in an amount that inhibits B-cell proliferation induced by IL-
CC 1Hv1. The method is useful for inhibiting or stimulating B-cell
CC proliferation, activation or differentiation in patients having a B-cell-
CC related disorder (e.g. lymphoma, leukemia, myeloma or infection) or an
CC autoimmune disease (e.g. allergy, asthma or allergic rhinitis), or in
CC screening for compounds that modulate B-cell differentiation. The IL-1Hv1
CC polypeptide, or the inhibitor of IL-1Hv1 activity, is useful in preparing
CC a medicament for stimulating or reducing B-cell proliferation.
CC differentiation or activation. The IL-1Hv1 polypeptide may also be used
CC in preparing a medicament for reducing IGA production
XX Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;
SQ Query Match 95.9%; Score 37.4; DB 8; Length 5751;
Best Local Similarity 97.4%; Pred. No. 0.00043;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTGAGGACAGCAGACTCCACAGCTCCCGCCAGGAGAA 39
DB 813 TGGAGGACAGCAGACTCCACAGCTCCCGCCAGGAGAA 851
RESULT 6
AAZ30052
ID AAZ30052 standard; DNA; 5752 BP.
XX AC AAZ30052;
XX 26-JAN-2000 (first entry)
XX DNA encoding a human interleukin-1 receptor antagonist.
XX Human; interleukin-1 receptor; IL-1; antagonist; sepsis;
KW acute pancreatitis; endotoxin shock; cytokine induced shock;
KW rheumatoid arthritis; chronic inflammatory arthritis;
KW pancreatic cell damage; diabetes mellitus type 1;
KW graft versus host disease; inflammatory bowel disease; inflammation;
KW pulmonary disease; autoimmune disease; inflammatory disease;
KW antiproliferative; myelogenous leukemia; premature labor;
KW intrauterine infection; nutritional activity;
KW hematopoiesis regulating activity; tissue growth activity;
KW activin activity; inhibin activity; chemotactic activity;
KW chemokinetic activity; hemostatic activity; thrombolytic activity;
KW anti-inflammatory activity; ss.
XX Homo sapiens.
XX WO9951744-A2.
XX 14-OCT-1999.
XX 05-APR-1999; 99WO-US004291.
XX 03-APR-1998; 98US-00055010.
PR 15-MAY-1998; 98US-00079909.
PR 20-MAY-1998; 98US-00082364.
PR 19-JUN-1998; 98US-00099818.
PR 31-JUL-1998; 98US-00127698.
PR 13-JAN-1999; 99US-00229591.
PR 17-FEB-1999; 99US-00251370.
XX (HYSE-) HYSEQ INC.
XX Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Ford J, Pace A, Alfenito M;
XX WPI; 1999-611042/52.

XX New isolated interleukin-1 receptor binding polypeptides, used to treat
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
 PT inflammatory disease, autoimmune disease or proliferative disease.
 XX
 PS Claim 1; Fig 9A-C; 123pp; English.
 XX
 CC The present sequence encodes a human interleukin-1 (IL-1) receptor
 CC antagonist. It represents the genomic sequence of AAZ30048-51. The
 CC encoded polypeptide is capable of binding IL-1 receptors (IL-1Rs). The
 CC polynucleotides and polypeptides can be used for the prevention or
 CC treatment of disorders involving sepsis, acute pancreatitis, endotoxin
 CC shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory
 CC arthritis, pancreatic cell damage from diabetes mellitus type 1, graft
 CC versus host disease, inflammatory bowel disease, inflammation associated
 CC with pulmonary disease, other autoimmune disease or inflammatory disease,
 CC an antiproliferative agent such as for acute or chronic myelogenous
 CC leukemia or in the prevention of premature labor secondary to
 CC intrauterine infections. They can also exhibit activities such as e.g.
 CC nutritional activity, cytokine and cell proliferation/differentiation
 CC activity, immune stimulating or suppressing activity, hematopoiesis
 CC regulating activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
 CC receptor/ligand activity, and anti-inflammatory activity. The products
 CC can also be used for detection, diagnosis and drug screening
 XX
 XX Sequence 5752 BP; 1467 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;

Query Match 95.9%; Score 37.4; DB 2; Length 5752;
 Best Local Similarity 97.4%; Pred. No. 0.00043;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGACAGGACGACTCCACAGCTCCCGCCAGGAGAA 39
 DB 813 TGGAGGACAGGACGACTCCACAGCTCCCGCCAGGAGAA 851

RESULT 7

AAZ27950
 ID AAF27950 standard; DNA; 6540 BP.

XX AAF27950;

XX 08-MAY-2001 (first entry)

XX Interleukin-1L1 genomic sequence.

XX Human; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
 KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
 KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
 KW osteoporosis; systemic lupus erythematosus; ds.

XX Unidentified.

XX WO200105974-A2.

XX 25-JAN-2001.

XX 17-JUL-2000; 2000WO-US019508.

XX 16-JUL-1999; 99US-0144298P.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Nicklin M, Barton J;

XX WPI; 2001-091974/10.

XX Nucleic acids encoding human and murine interleukin-1L1 polypeptides
 PT useful for controlling inflammatory processes.

XX Example; Fig 11; 150pp; English.

XX

CC The present invention provides the protein and coding sequences of the
 CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
 CC located between the IL-1beta and IL-1receptor genes at human chromosome
 CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
 CC of heart disease, cancer and inflammatory diseases such as rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
 CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
 CC severe periodontal disease and pregnancy complications. The present
 CC sequence is the IL-1L1 gene

XX Sequence 6540 BP; 1747 A; 1458 C; 1709 G; 1626 T; 0 U; 0 Other;

Query Match 95.9%; Score 37.4; DB 5; Length 6540;
 Best Local Similarity 97.4%; Pred. No. 0.00044;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGACAGGACGACTCCACAGCTCCCGCCAGGAGAA 39
 DB 970 TGGAGGACAGGACGACTCCACAGCTCCCGCCAGGAGAA 1008

RESULT 8

AAZ30053

ID AAZ30053 standard; DNA; 7605 BP.

XX AAZ30053;

XX 26-JAN-2000 (first entry)

XX DNA encoding a human interleukin-1 receptor antagonist.

XX Human; interleukin-1 receptor; IL-1; antagonist; sepsis;
 KW acute pancreatitis; endotoxin shock; cytokine induced shock;
 KW rheumatoid arthritis; chronic inflammatory arthritis;
 KW pancreatic cell damage; diabetes mellitus type 1;
 KW graft versus host disease; inflammatory bowel disease; inflammation;
 KW pulmonary disease; autoimmune disease; inflammatory disease;
 KW antiproliferative; myelogenous leukemia; premature labor;
 KW intrauterine infection; nutritional activity;
 KW hematopoiesis regulating activity; tissue growth activity;
 KW activin activity; inhibin activity; chemotactic activity;
 KW chemokinetic activity; hemostatic activity; thrombolytic activity;
 KW anti-inflammatory activity; ss.

XX Homo sapiens.

XX WO9951744-A2.

XX 14-OCT-1999.

XX 05-APR-1999; 99WO-US004291.

XX 03-APR-1998; 98US-00055010.

XX 15-MAY-1998; 98US-00079909.

XX 20-MAY-1998; 98US-00082364.

XX 19-JUN-1998; 98US-00099818.

XX 31-JUL-1998; 98US-00127698.

XX 13-JAN-1999; 99US-00229591.

XX 17-FEB-1999; 99US-00251370.

XX (HYGE-) HYSEQ INC.

XX Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;

XX Leshkowitz D, Kita D, Ford J, Pace A, Alfinito M;

XX WPI; 1999-611042/52.

XX New isolated interleukin-1 receptor binding polypeptides, used to treat
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
 PT inflammatory disease, autoimmune disease or proliferative disease.
 XX Disclosure; Fig 10A-C; 123pp; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
CC represent sequences used in the exemplification of the present invention
XX

Seq Sequence 689 BP; 138 A; 193 C; 207 G; 143 T; 0 U; 8 Other;

Query Match 57.4%; Score 22.4; DB 4; Length 689;
Best Local Similarity 81.2%; Pred. No. 1.3e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TTGAGGACAGGACGACTCCACAGCTCCCGCC 32
DB 486 TTGAGGACATGAGATCCACAGCTCTCGCC 455

RESULT 14
AA527743
ID AAS27743 standard; DNA; 7667 BP.
AC AAS27743;
XX
XX
XX 07-NOV-2001 (first entry)
DE
DE DNA encoding novel signal transduction pathway protein, Seq ID 1403.
XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS; ds;
XX acquired immune deficiency syndrome.
XX Homo sapiens.
XX
XX WO20015733-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US0001312.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 14-SEP-2000; 2000US-0232399P.
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PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246527P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX Claim 1; SEQ ID NO 1403; 880pp; English.
XX The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
CC AAS27850 represent novel signal transduction pathway protein coding
CC sequences and PCR primers of the invention
XX
SQ Sequence 7667 BP; 1717 A; 2370 C; 2150 G; 1430 T; 0 U; 0 Other;
Query Match 57.4%; Score 22.4; DB 4; Length 7667;
Best Local Similarity 81.2%; Pred. No. 1.7e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TTGAGGACAGGACAGCTCCAGCTCCGCCC 32
DB 809 TTGGGGACATGCAGAAATCCAGCTCTCGCC 840
RESULT 15
AAK82163/c
ID AAK82163 standard; DNA; 7667 BP.
XX
AC AAK82163;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36975.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189674P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 11-JUL-2000; 2000US-0217487P.
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PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.
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PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 05-JAN-2001; 2000US-0259678P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.

XX Disclosure; SEQ ID NO 36975; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
CC represent sequences used in the exemplification of the present invention
XX

SQ Sequence 7667 BP; 1430 A; 2150 C; 2370 G; 1717 T; 0 U; 0 Other;

Query Match 57.4%; Score 22.4; DB 4; Length 7667;
Best Local Similarity 81.2%; Pred. NO. 1.7e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTGAGGACAGGACATCCACAGCTCCGCC 32
|||||

Db 6859 TTGGGGACATGCAGATCCACAGCTCTCGCC 6828

Search completed: March 13, 2005, 12:34:17
Job time : 27.9367 secs

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